

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2003, 22:58:15 : Search time 142 Seconds

(without alignments)
6216.664 Million cell updates/sec

Title: US-09-977-260-1

Perfect score: 2000

Sequence: 1 ctcgctcaagtggtgcagc.....attctaaggaacttaaaaa 2000

Scoring table: IDENTITY-NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_NA.*
2: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2000	100.0	2000	US-08-426-509A-1	Sequence 1, Appli
2	2000	100.0	2000	US-08-232-545-1	Sequence 1, Appli
3	2000	100.0	2000	PCT-US95-05008-1	Sequence 1, Appli
4	1909.8	95.5	1987	US-08-876-882-1	Sequence 1, Appli
5	1909.8	95.5	1987	US-09-315-928-1	Sequence 1, Appli
6	1903.4	95.2	1942	US-08-604-989A-11	Sequence 11, Appli
7	1519.4	76.0	1521	US-08-604-989A-10	Sequence 10, Appli
8	1398	69.9	1398	US-08-604-989A-9	Sequence 9, Appli
9	1377	68.8	1713	US-09-741-154-1	Sequence 1, Appli
10	738	36.9	738	US-08-604-989A-8	Sequence 8, Appli
11	455	22.8	16389	US-09-741-154-3	Sequence 3, Appli
12	225	11.2	225	US-08-604-989A-7	Sequence 7, Appli
13	212.4	10.6	1611	US-07-820-011A-3	Sequence 3, Appli
14	212.4	10.6	1611	PCT-US93-00445-3	Sequence 3, Appli
15	199.2	10.0	1602	US-07-820-011A-1	Sequence 1, Appli
16	199.2	10.0	1602	PCT-US93-00445-1	Sequence 1, Appli
17	192	9.6	192	US-08-604-989A-6	Sequence 6, Appli
18	185	9.2	1574	US-09-173-581-12	Sequence 12, Appli
19	185	9.2	1574	US-09-420-915-12	Sequence 12, Appli
20	181.8	9.1	3623	US-08-306-691B-35	Sequence 35, Appli
21	170.4	8.5	1467	US-09-579-182-2	Sequence 2, Appli
22	168.8	8.4	1458	US-09-099-053-1	Sequence 1, Appli
23	165.8	8.3	2674	US-09-817-180-1	Sequence 1, Appli
24	162	8.1	5993	US-09-383-630-1	Sequence 1, Appli
25	162	8.1	5993	US-09-383-630-2	Sequence 2, Appli
26	151.2	7.6	2647	US-09-220-132-77	Sequence 77, Appli
27	151.2	7.6	2647	PCT-US93-06251-77	Sequence 77, Appli

28	148.8	7.4	2049	US-09-099-749-10
29	148.8	7.4	2433	US-09-620-312D-830
30	148.8	7.4	2598	US-09-417-197-110
31	148.8	7.4	2616	US-09-417-197-108
32	148	7.4	2469	US-08-459-236-1
33	146.4	7.3	933	US-08-701-191A-4
34	146.4	7.3	1056	US-08-701-191A-5
35	146.4	7.3	2469	US-07-997-133-2
36	146.4	7.3	2469	US-07-997-133-2
37	146.4	7.3	2662	US-08-451-822A-14
38	146.4	7.3	2662	US-08-323-430-14
39	146.4	7.3	2733	US-08-371-001-14
40	146.4	7.3	2733	PCT-US96-00331-14
41	137.6	6.9	1491	US-09-006-675-1
42	137.6	6.9	1491	US-09-228-603A-1
43	136.6	6.8	3945	US-09-016-434-1404
44	136.6	6.8	3969	US-08-436-044-5
45	136.6	6.8	3969	US-08-222-616-23

ALIGNMENTS

RESULT 1
US-08-426-509A-1
Sequence 1, Application US/08426509A

Patent No. 6326469

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel

APPLICANT: Gishizky, Mikhail

APPLICANT: Sures, Irman G.

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN

TITLE OF INVENTION: TYROSINE KINASES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penne & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York,

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTED Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A

FILING DATE: 21-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/232,545

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-0074-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2000 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

US-08-426-509A-1

Sequence 10, Appli
Sequence 830, App
Sequence 110, App
Sequence 108, App
Sequence 1, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1404, Ap
Sequence 5, Appli
Sequence 23, Appli

Query Match 100.0% Score 2000, DB 4, Length 2000;
Best Local Similarity 100.0% Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Gaps 0;

TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,545
FILING DATE: 22-Apr-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)90-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2000 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-08-232-545-1

Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCCCAAGTTGTGACGCGGAGACCGCTCGGGGTGTGACGCGCGGTCCGAGAGCCC 60
Db 1 CTCCTCTCCAGTTGTGTGACGCGGAGACCGCTCGGGGTGTGACGCGCGGTCCGAGAGCCC 60
QY 61 TCCTGAGGAGGCGGCGGCGGCGCTCGGGGCGGCCCTGAGCAAAAAAGGAAGAAC 120
Db 61 TCCTGAGGAGGCGGCGGCGGCGCTCGGGGCGGCCCTGAGCAAAAAAGGAAGAAC 120
QY 121 AGGCTGGTCCAGTGGGACCCAGCTCCCTACCTCTGTGACGCGCGCTGGCTGTGCA 180
Db 121 AGGCTGGTCCAGTGGGACCCAGCTCCCTACCTCTGTGACGCGCGCTGGCTGTGCA 180
QY 181 GGGCATTCGCGGCTGCCCGGAGTGAACACTTGTGAGTGGCTCTCAGCTGCTCAGT 240
Db 181 GGGCATTCGCGGCTGCCCGGAGTGAACACTTGTGAGTGGCTCTCAGCTGCTCAGT 240
QY 241 TTTCCTCTGTGGGGGCGATGGGCGGAGGCTCTGTGTTCTCTGGGGGCGATTTCAG 300
Db 241 TTTCCTCTGTGGGGGCGATGGGCGGAGGCTCTGTGTTCTCTGGGGGCGATTTCAG 300
QY 301 GCTGTGATTCTGTGAGGAATTCGCCGGGTGAGCCCCCGTTCTCCGAGCTTGGAC 360
Db 301 GCTGTGATTCTGTGAGGAATTCGCCGGGTGAGCCCCCGTTCTCCGAGCTTGGAC 360
QY 361 CCCCTCCGTTGACGAGATGCAAGAGAGGCGCTGGGCGCGGCGACCCAGTGTATCA 420
Db 361 CCCCTCCGTTGACGAGATGCAAGAGAGGCGCTGGGCGCGGCGACCCAGTGTATCA 420
QY 421 CCAATGAGAGCACACCGCGCCCAAGCAGAGGAGTGGCTTCCGCAAGGGCGACGTGG 480
Db 421 CCAATGAGAGCACACCGCGCCCAAGCAGAGGAGTGGCTTCCGCAAGGGCGACGTGG 480
QY 481 TCACCATCTGTGAGGCTGCGAGAACAGAGCTGTGACCGGCTGAAGCACCACCACTG 540
Db 481 TCACCATCTGTGAGGCTGCGAGAACAGAGCTGTGACCGGCTGAAGCACCACCACTG 540

Db 481 TCACCATCTGTGAGGCTGCGAGAACAGAGCTGTGACCGGCTGAAGCACCACCACTG 540
QY 541 GACAGAGAGGCTGTGTGACACTGGGGGCGTTCGCGGAGCGGAGGCCCTCTCCGAGACC 600
Db 541 GACAGAGAGGCTGTGTGACACTGGGGGCGTTCGCGGAGCGGAGGCCCTCTCCGAGACC 600
QY 601 CCAAGCTAGGCTCATGCGCGGTTCACGGGAAGATCTCGGCGCAGAGAGCTGTCCAGC 660
Db 601 CCAAGCTAGGCTCATGCGCGGTTCACGGGAAGATCTCGGCGCAGAGAGCTGTCCAGC 660
QY 661 AGCTGACGCTCCCGAGGATGGGCTTCTGTGCGGAGAGTCCGCGGCCACCCCGGCG 720
Db 661 AGCTGACGCTCCCGAGGATGGGCTTCTGTGCGGAGAGTCCGCGGCCACCCCGGCG 720
QY 721 ACTAGCTGTGCGTGTGAGCTTTGGCGCGAGCTCATCATCTACCGGCTGTCTGACCCG 780
Db 721 ACTAGCTGTGCGTGTGAGCTTTGGCGCGAGCTCATCATCTACCGGCTGTCTGACCCG 780
QY 781 ACGGCGACCTACATCGATGAGCGCGTTCCTTCGACCTCATGGAATGTGGAGC 840
Db 781 ACGGCGACCTACATCGATGAGCGCGTTCCTTCGACCTCATGGAATGTGGAGC 840
QY 841 ATTACAGCAAGAGCAAGGGCGCTATCTGCACCAAGCTGTGAGACCAAAAGCGAAACAG 900
Db 841 ATTACAGCAAGAGCAAGGGCGCTATCTGCACCAAGCTGTGAGACCAAAAGCGAAACAG 900
QY 901 GGACCAATCGGCGGAGAGAGCTGGCGCAGGGCGGCTGTACTGAACCTGTGACGACT 960
Db 901 GGACCAATCGGCGGAGAGAGCTGGCGCAGGGCGGCTGTACTGAACCTGTGACGACT 960
QY 961 TGACATTGGAGACAGATCGAGAGAGAGATTGGAGCTGTCTGACAGGTTGAGTACC 1020
Db 961 TGACATTGGAGACAGATCGAGAGAGAGATTGGAGCTGTCTGACAGGTTGAGTACC 1020
QY 1021 TGGGCAAAAGGTGGCGCTGAAGAAATATCAAGTGTGATGACAGCCAGGCTTCTG 1080
Db 1021 TGGGCAAAAGGTGGCGCTGAAGAAATATCAAGTGTGATGACAGCCAGGCTTCTG 1080
QY 1081 ACGAGACGGCGCTATGACGAAGATGCAACAGCAACCTGTGTGCTCTCGGGCGTGA 1140
Db 1081 ACGAGACGGCGCTATGACGAAGATGCAACAGCAACCTGTGTGCTCTCGGGCGTGA 1140
QY 1141 TCCTGACACAGGGGCTGTACATTTGTCAATGAGACAGTGAAGGGCAACCTGTGAACT 1200
Db 1141 TCCTGACACAGGGGCTGTACATTTGTCAATGAGACAGTGAAGGGCAACCTGTGAACT 1200
QY 1201 TTCTGCGAGCCCGGGGCTGAGCCCTGTGAACACCGCTACGCTCTGTGAGTTTCTG 1260
Db 1201 TTCTGCGAGCCCGGGGCTGAGCCCTGTGAACACCGCTACGCTCTGTGAGTTTCTG 1260
QY 1261 ACGTGGCGGAGGGCATGTGAGTACCTGAGACCAAGACTGTGTGACCGGCACTGGGCG 1320
Db 1261 ACGTGGCGGAGGGCATGTGAGTACCTGAGACCAAGACTGTGTGACCGGCACTGGGCG 1320
QY 1321 CCCGCAATCTGTGTCACAGAGCACTGTGGGCGCAAGGTGACGCACTTTGGCGTGGCA 1380
Db 1321 CCCGCAATCTGTGTCACAGAGCACTGTGGGCGCAAGGTGACGCACTTTGGCGTGGCA 1380
QY 1381 AAGCCGAGCGGAAGGGGCTAGACTCAAGCCGAGTCCCGCTCAAGTGAAGCGGCGCGAG 1440
Db 1381 AAGCCGAGCGGAAGGGGCTAGACTCAAGCCGAGTCCCGCTCAAGTGAAGCGGCGCGAG 1440
QY 1441 CTCCTCAACACAGGGGAAGTTCAACAGCAAGTGGAGTGTGTGAGTTTGGGGTGTGCT 1500
Db 1441 CTCCTCAACACAGGGGAAGTTCAACAGCAAGTGGAGTGTGTGAGTTTGGGGTGTGCT 1500
QY 1501 GGGAGGCTTCTCAATATGAGAGGCTCCGTACCTCAATATGTCACTGAAGAAGGTGTGG 1560
Db 1501 GGGAGGCTTCTCAATATGAGAGGCTCCGTACCTCAATATGTCACTGAAGAAGGTGTGG 1560
QY 1561 AGGCGGTGAGAGAGGGGTACCGCATGGAACCCCGGAGGCTGTCCAGGCCCGCTGACG 1620
Db 1561 AGGCGGTGAGAGAGGGGTACCGCATGGAACCCCGGAGGCTGTCCAGGCCCGCTGACG 1620

QY	1621	TCCTCATGAGCAGCTGCTGGGGAGGACAGACCCCGCCGACCCCTTCGCGAACTGG	1680
Db	1621	TCCTCATGAGCAGCTGCTGGGGAGGACAGACCCCGCCGACCCCTTCGCGAACTGG	1680
QY	1681	CCGAGAAAGCTGGCCCGGAGCTACGCAGTGCAGGTGCCCCAGCCTCGTCTCAGGGCAGG	1740
Db	1681	CCGAGAAAGCTGGCCCGGAGCTACGCAGTGCAGGTGCCCCAGCCTCGTCTCAGGGCAGG	1740
QY	1741	ACGCGCAGCGGCTTCCACCTCGCCCGGAAAGCCAGAGGACCCCTGACCCCGGTGGGGGCGCT	1800
Db	1741	ACGCGCAGCGGCTTCCACCTCGCCCGGAAAGCCAGAGGACCCCTGACCCCGGTGGGGGCGCT	1800
QY	1801	TGGCCCCAGAGAGCAGAGAGAGTGGAGAGTGGCGGCGTGGGGGCGACTGACCAAGGCCAAGG	1860
Db	1801	TGGCCCCAGAGAGCAGAGAGAGTGGAGAGTGGCGGCGTGGGGGCGACTGACCAAGGCCAAGG	1860
QY	1861	AGGGTCCAGCGGGGCGCAAGTATCTCTCTGTTGCCACAGCAGGGGGCTGGCCACGTAGGG	1920
Db	1921	GGGCTCTGGGGCGGCCGCTGGACACACCCAGACCTGGGAGGATGATCGCCGATAAAGCAGG	1980
QY	1921	GGGCTCTGGGGCGGCCGCTGGACACACCCAGACCTGGGAGGATGATCGCCGATAAAGCAGG	1980
Db	1921	GGGCTCTGGGGCGGCCGCTGGACACACCCAGACCTGGGAGGATGATCGCCGATAAAGCAGG	1980
QY	1981	ATTCTAAGGACTTAATAAAA 2000	
Db	1981	ATTCTAAGGACTTAATAAAA 2000	

RESULT 3
PCT-US95-05008-1

Sequence 1, Application PC/TUS9505008

GENERAL INFORMATION:

APPLICANT: Sugen, Inc.

APPLICANT: 515 Galveston Drive

APPLICANT: Redwood City, California 94063-4720

APPLICANT: United States of America

APPLICANT: Wissenschaften E.V.

APPLICANT: Hofgarten Str. 2

APPLICANT: Munchen 80539

APPLICANT: Germany

TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05008

FILING DATE: 24-APR-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/232,545

FILING DATE: 22-APR-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-074

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9050

TELEFAX: (212)869-9741

TELEX: 66141 PENNIE

```

? INFORMATION FOR SEQ ID NO: 1:
?
?   SEQUENCE CHARACTERISTICS:
?       LENGTH: 2000 base pairs
?       type: nucleic acid
?       STRANDEDNESS: unknown
?       TOPOLOGY: unknown
?       MOLECULE TYPE: DNA
?   PCT-US95-05008-1

```

Query Match	100.0%	Score 2000;	DB 5;	Length 2000;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	CTCCCTCAAGTTTGTGACAGCGGGAACCGCTCTGGGGGTGTGCAAGCGGCTCCGGAAGGCC	60
Db	1	CTGCCTCAAGTTTGTGACGCCGGGAACCGCTCTGGGGGTGTGCAAGCGGCTCCGGAAGGCC	60
QY	61	TCCTGGGGGGGGCGGGGGGGCTCGGGGGGGCCCCTGAGCAAAAACAGAAAGAC	120
Db	61	TCCTGGGGGGGGGGGGGGGGGGCTCGGGGGGGGGCCCCTGAGCAAAAACAGAAAGAC	120
QY	121	AGGCTGGGTCCAGTGGGACCAGTCCCTACTCTGTGGCAGGCGGCTGGACTGTGGCA	180
Db	121	AGGCTCGGTCCAGTGGCAACCAGTCCCTACTCTGTGGCAGGCGGCTGGACTGTGGCA	180
QY	181	GGCCATTCCAGAGCTCCCGACTGTGACCACTTGCTCAGTGGCTCTCACCTGCCTAG	240
Db	181	GGCCATTCCAGAGCTCCCGACTGTGACCACTTGCTCAGTGGCTCTCACCTGCCTAG	240
QY	241	TTTTCCCTGGGGGGGCGATGGCGGGGGAGGCTCTGTGGTTTCCGTGGCGGGCAATTTACG	300
Db	241	TTTTCCCTGTGGGGGGCATGGCGGGGGAGGCTCTGTGGTTTCTGTGGGGCAATTTACG	300
QY	301	GCTGTGATTTGCTGAGGAACTTTCCCGGGGTGAGCCCGCTCTCTCGAGACTTGGAC	360
Db	301	GCTGTGATTTGCTGAGGAACTTTCCCGGGGTGAGCCCGCTCTCTCGAGACTTGGAC	360
QY	361	CCCTCTCCCTCTCAGCCAGATGCCAAAGAGGCGCTGGGCCCGGGGCAACCAATGTATCA	420
Db	361	CCCTCTCCCTCTCAGCCAGATGCCAAAGAGGCGCTGGGCCCGGGGCAACCAATGTATCA	420
QY	421	CCAAATCGAGACACACCCGCCCAAGCAGGGGAGCTGGCTTTCCGCAAGGGGCAAGCTGG	480
Db	421	CCAAATCGAGACACACCCGCCCAAGCAGGGGAGCTGGCTTTCCGCAAGGGGCAAGCTGG	480
QY	481	TCACCATCTGTGAGAGCCTGCGAAGAAAGAGCTGTACCGGTCAGACACCAACCAAGTG	540
Db	481	TCACCATCTGTGAGAGCCTGCGAAGAAAGAGCTGTACCGGTCAGACACCAACCAAGTG	540
QY	541	GACAGAGAGGGGCTGTGGACGTGGGGGCGCTGGCGGGAGCGGAGGCCCTCTCCGCAAGC	600
Db	541	GACAGAGAGGGGCTGTGGACGTGGGGGCGCTGGCGGGAGCGGAGGCCCTCTCCGCAAGC	600
QY	601	CCAAGCTCACGCTCATGCGCTGTGTTTCCACGGGAAGATCTGGGCGCAGGAGGCTTCCAGC	660
Db	601	CCAAGCTCACGCTCATGCGCGTGTGTTTCCACGGGAAGATCTGGGCGCAGGAGGCTTCCAGC	660
QY	661	AGCTGCAGGCTCCCGAAGATGGGCTGTGTTCTGTGGGTGAGTCCGCGCCGACCCCGGCG	720
Db	661	AGCTGCAGGCTCCCGAAGATGGGCTGTGTTCTGTGGGTGAGTCCGCGCCGACCCCGGCG	720
QY	721	ACTACGATCGTGGGTGAGCTTTTGGCGCGCAGCTATCCACTACGGGTGCTGCAACGGCG	780
Db	721	ACTACGATCTGTGGGTGAGCTTTTGGCGCGCAGCTATCCACTACGGGTGCTGCAACGGCG	780
QY	781	ACGGCCACTTCACAAATGATGAGGCGGTGTTCTGCTCAACCTTATGAGACATGGTGAAGC	840
Db	781	ACGGCCACTTCACAAATGATGAGGCGGTGTTCTGCTCAACCTTATGAGACATGGTGAAGC	840
QY	841	ATTACAGCAGAGCAGAGGGGCGTATCTGCAACCAAGCTGTGTAGACCAAAGCGGAACAGC	900
Db	841	ATTACAGCAGAGCAGAGGGGCGTATCTGCAACCAAGCTGTGTAGACCAAAGCGGAACAGC	900

QY 901 GGACCAAGTCGGCCGAGGAGGAGCTGGCCAGGGCGGGCTGGTACTGAACTGCAGCAT 960
 Db 901 GGACCAAGTCGGCCGAGGAGGAGCTGGCCAGGGCGGGCTGGTACTGAACTGCAGCAT 960
 QY 961 TGACATTGGGAGCAGATGAGGAGGAGGAGTGGAGCTGTCCTGACGGTGCAGTACC 1020
 Db 961 TGACATTGGGAGCAGATGAGGAGGAGGAGTGGAGCTGTCCTGACGGTGCAGTACC 1020
 QY 1021 TGGGGCAAAAGTGGCCGTGAAAGATATCAAGTGTGATGACAGCCAGCCCTTCTGG 1080
 Db 1021 TGGGGCAAAAGTGGCCGTGAAAGATATCAAGTGTGATGACAGCCAGCCCTTCTGG 1080
 QY 1081 ACAGAGAGCGGCTGATGACGAGAGATGACAGAGAACTGTGGCTCTCTGGGCGTGA 1140
 Db 1081 ACAGAGAGCGGCTGATGACGAGAGATGACAGAGAACTGTGGCTCTCTGGGCGTGA 1140
 QY 1141 TCCTGACCAAGGGGCTGTATATGTCATGAGACAGCGTGAAGGGCAACCTGGTGAAT 1200
 Db 1141 TCCTGACCAAGGGGCTGTATATGTCATGAGACAGCGTGAAGGGCAACCTGGTGAAT 1200
 QY 1201 TTCTGGGACCCGGGGTGCAGCCCTGTAACACCCGCTCAGCTCTGAGTTTCTCTGC 1260
 Db 1201 TTCTGGGACCCGGGGTGCAGCCCTGTAACACCCGCTCAGCTCTGAGTTTCTCTGC 1260
 QY 1261 ACGTGGCCGAGGGCATGAGTACCTGGAGAGCAAGAACTGTGACACCGGACCTGGCCG 1320
 Db 1261 ACGTGGCCGAGGGCATGAGTACCTGGAGAGCAAGAACTGTGACACCGGACCTGGCCG 1320
 QY 1321 CCGGCAACATCTCTGTCTCAGAGGAGCTGGTGGCCAAAGTTCAGAGACTTTGGCCTGCCA 1380
 Db 1321 CCGGCAACATCTCTGTCTCAGAGGAGCTGGTGGCCAAAGTTCAGAGACTTTGGCCTGCCA 1380
 QY 1381 AAGCCGAGCGGAAGGGCTGAGTCAAGCCGGCTGACCTCAAGTGGAGCGGCGCCGAGG 1440
 Db 1381 AAGCCGAGCGGAAGGGCTGAGTCAAGCCGGCTGACCTCAAGTGGAGCGGCGCCGAGG 1440
 QY 1441 CTCTCAAAACACGGGAAGTTTACCAGCAAGTGTGATGTTTGGGGTGTGCTCT 1500
 Db 1441 CTCTCAAAACACGGGAAGTTTACCAGCAAGTGTGATGTTTGGGGTGTGCTCT 1500
 QY 1501 GGGAGGTCTTCTATATGAGCGGGCTCCGTAACCTAAATGTCACTGAAAGAGGTGTGCG 1560
 Db 1501 GGGAGGTCTTCTATATGAGCGGGCTCCGTAACCTAAATGTCACTGAAAGAGGTGTGCG 1560
 QY 1561 AGGCGGTGAGAAAGGGGTACCGATGAGAACCCCGGAGGGCTGTCCAGGCCCGGTGCACG 1620
 Db 1561 AGGCGGTGAGAAAGGGGTACCGATGAGAACCCCGGAGGGCTGTCCAGGCCCGGTGCACG 1620
 QY 1621 TCCTCATGAGCAGCTGCTGGAGGAGCAGAGCCCGCCGCGCAACCTTCCGAAACTGG 1680
 Db 1621 TCCTCATGAGCAGCTGCTGGAGGAGCAGAGCCCGCCGCGCGCAACCTTCCGAAACTGG 1680
 QY 1681 CCGAGAAAGTGGCCCGGAGCTACGAGTGCAGGTGCCCCAGCCTCCGTCTCAGGGCAGG 1740
 Db 1681 CCGAGAAAGTGGCCCGGAGCTACGAGTGCAGGTGCCCCAGCCTCCGTCTCAGGGCAGG 1740
 QY 1741 AGCGCGAGGCTCACCTGCGCCCGAAGCCAGAGGCCCTGACCCCAACCGGTGGGGCCT 1800
 Db 1741 AGCGCGAGGCTCACCTGCGCCCGAAGCCAGAGGCCCTGACCCCAACCGGTGGGGCCT 1800
 QY 1801 TGGCCCCAGAGACCGAGAGAGTGCAGGTGCGGGGCGCACTGACCAAGGCCCAAGG 1860
 Db 1801 TGGCCCCAGAGACCGAGAGAGTGCAGGTGCGGGGCGCACTGACCAAGGCCCAAGG 1860
 QY 1861 AGGGTCCAGGCGGGCAAGTATCTCTGTTGCCACAGCAGGAGGCGCTGAGGTAGG 1920
 Db 1861 AGGGTCCAGGCGGGCAAGTATCTCTGTTGCCACAGCAGGAGGCGCTGAGGTAGG 1920
 QY 1921 GGGTCTGGGCGGCGGAGACCCAGACCTGGAAGGATGATGCCCAATAAGACGG 1980
 Db 1921 GGGTCTGGGCGGCGGAGACCCAGACCTGGAAGGATGATGCCCAATAAGACGG 1980
 QY 1981 ATTCTAAGACTCTAAAAA 2000

Db 1981 ATTCTAAGACTCTAAAAA 2000
 RESULT 4
 US-08-876-882-1
 ; Sequence 1, Application US/08876882
 ; Patent No. 5981201
 ; GENERAL INFORMATION:
 ; APPLICANT: Abraham, Hava
 ; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173-4799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/876,882
 ; FILING DATE: 16-JUN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/035,228
 ; FILING DATE: 08-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Doreen, Hogle M
 ; REGISTRATION NUMBER: 36,361
 ; REFERENCE/DOCKET NUMBER: NED97-01pa
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 781-861-6240
 ; TELEFAX: 781-861-9540
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1987 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-876-882-1
 Query Match 95.5%; Score 1909.8; DB 2; Length 1987;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1973; Conservative 0; Mismatches 7; Indels 9; Gaps 5;
 QY 1 CTCGCTCAAGATTGTGACGCGGAGCCGCTCGGGGTGTGACAGCGGCTGCGGAGGCC 60
 Db 8 CTCGCTCAAGATTGTGACGCGGAGCCGCTCGGGGTGTGACAGCGGCTGCGGAGGCC 67
 QY 61 TCTGG 120
 Db 68 TCTGG 127
 QY 121 AGGCTGCTCAGTGGGACGACGCTCCTACCTCTGTCGAGCGGCTGGCTGTGGA 180
 Db 128 AGGCTGCTCAGTGGGACGACGCTCCTACCTCTGTCGAGCGGCTGGCTGTGGA 187
 QY 181 GGGCATTCCAGCGTCCCGCACTGTGACACCTTGCTAGTGTGCTCTCACTGCTCAG 240
 Db 188 GGCATTCACAGCGTCCCGCACTGTGACACCTTGCTAGTGTGCTCTCACTGCTCAG 247
 QY 241 TTTCCCTCTGGGGGGGCGATGGCGGGGAGAGGCTCTGTGTTTCTGGCGGGCATTTACG 300
 Db 248 TTTCC--TCTGGGGGCGATGGCGGGGAGAGGCTCTGTGTTTCTGGCGGGCATTTACG 305

QY 301 GCTGATTTCTGTAGAGACTTCCCGGGTGTAGCCGCCCTTCTCTCCGAGCTGTGGCAC 360
 Db 306 GCTGATTTCTGTAGAGACTTCCCGGGTGTAGCCGCCCTTCTCTCCGAGCTGTGGCAC 365
 QY 361 CCCCTCCCGTCTCAGCAGAGATGCAACAGAGCGCTGGGCCCCGGGACCCCGTGTATCA 420
 Db 366 CCCCTCCCGTCTCAGCAGAGATGCAACAGAGCGCTGGGCCCCGGGACCCCGTGTATCA 425
 QY 421 CCAATGCGAGACACCCGCCCAAGCCAGGGGAGCTGGCTTCCGCAAGGGCGAGCTGG 480
 Db 426 CCAATGCGAGACACCCGCCCAAGCCAGGGGAGCTGGCTTCCGCAAGGGCGAGCTGG 485
 QY 481 TCACCATCTGTAGAGCTGTCGAGAACAGAGCTGTACCGGTCAAGACACACAGTGTG 540
 Db 486 TCACCATCTGTAGAGCTGTCGAGAACAGAGCTGTACCGGTCAAGACACACAGTGTG 545
 QY 541 GACAGAGAGGGGTGTGTGAGCTGGGGGCTGCGGAGGGGAGGCGCTCTCCGAGACC 600
 Db 546 GACAGAGAGGGGTGTGTGAGCTGGGGGCTGCGGAGGGGAGGCGCTCTCTCCGAGACC 605
 QY 601 CCAAGCTCAGCCCTCATGCGCTGTTCACAGGGGAGATCTCGGGCCAGGAGGCTGTCAAC 660
 Db 606 CCAAGCTCAGCCCTCATGCGCTGTTCACAGGGGAGATCTCGGGCCAGGAGGCTGTCAAC 665
 QY 661 AGCTGACACCTCCGAGAGATGGGCTGTCTGTGTCGGGAGTCCGGCCGACCCCGGCG 720
 Db 666 AGCTGACACCTCCGAGAGATGGGCTGTCTGTGTCGGGAGTCCGGCCGACCCCGGCG 725
 QY 721 ACTAGCTCTGTGCTGTGAGCTTTGGCCGAGCTGATCATACCGGCTGTGTCAGCCGG 780
 Db 726 ACTAGCTCTGTGCTGTGAGCTTTGGCCGAGCTGATCATACCGGCTGTGTCAGCCGG 785
 QY 781 ACGGCGACCTCACAATGATGAGGCGGTGTCTTCTGCAACCTCATGAGCATGTGAGAC 840
 Db 786 ACGGCGACCTCACAATGATGAGGCGGTGTCTTCTGCAACCTCATGAGCATGTGAGAC 845
 QY 841 ATTACAGAGAGAACAGGGGCGCTATCTGTACCAACCTGTGTGAGACCAAGCGAAGACG 900
 Db 846 ATTACAGAGAGAACAGGGGCGCTATCTGTACCAACCTGTGTGAGACCAAGCGAAGACG 905
 QY 901 GGACCAAGTGGGCGAGGAGAGAGCTGGCCAGGGCGGTGTACTGAACCTGACGACATT 960
 Db 906 GGACCAAGTGGGCGAGGAGAGAGCTGGCCAGGGCGGTGTACTGAACCTGACGACATT 965
 QY 961 TGACATTGGGAGACACAGATCGAGAGGAGAGATTGAGCTGTCTGCAAGGGTGAATAC 1020
 Db 966 TGACATTGGGAGACACAGATCGAGAGGAGAGATTGAGCTGTCTGCAAGGGTGAATAC 1025
 QY 1021 TGGGCGCAAAAGTGGCCGTGAAGATATCAAGTGTGATGTGACACCCAGGGCTTCTGG 1080
 Db 1026 TGGGCGCAAAAGTGGCCGTGAAGATATCAAGTGTGATGTGACACCCAGGGCTTCTGG 1085
 QY 1081 ACGAGAGCGGCGTGTATGAGAGATGCAACAGAGACCTGGTGGCTTCTCTGGGCGTGA 1140
 Db 1086 ACGAGAGCGGCGTGTATGAGAGATGCAACAGAGACCTGGTGGCTTCTCTGGGCGTGA 1145
 QY 1141 TCTGTGACCAAGGGGCTGTATGATGTGATGAGACAGCTGAGCAAGGGCAACCTGTGAAT 1200
 Db 1146 TCTGTGACCAAGGGGCTGTATGATGTGATGAGACAGCTGAGCAAGGGCAACCTGTGAAT 1205
 QY 1201 TTTGTGCGAGCCGGGGTGTGAGCCCTCGTGAACACCGCTCAGTCTCTGAGTTTCTGTGC 1260
 Db 1206 TTTGTGCGAGCCGGGGTGTGAGCCCTCGTGAACACCGCTCAGTCTCTGAGTTTCTGTGC 1265
 QY 1261 ACGTGGCGAGGCGATGAGTACCTGGAGAGCAAGAACTGTGTGACCGCGACCTGGGCG 1320
 Db 1266 ACGTGGCGAGGCGATGAGTACCTGGAGAGCAAGAACTGTGTGACCGCGACCTGGGCG 1325
 QY 1321 CCGGCAACATCTGTGTCAGAGAGACCTGTGTGCGCAAGGTGACGACTTTGGCGTGGCA 1380
 Db 1326 CCGGCAACATCTGTGTCAGAGAGACCTGTGTGCGCAAGGTGACGACTTTGGCGTGGCA 1385
 QY 1381 AAGCGAGCGGAGAGGGGCTAGACATCAAGCCGGCTGCCCTCAAGTGAAGCGGCGCCGAGG 1440

Db 1386 AAGCGAGCGGAGAGGGCTAGACTCAAGCCGGCTGCGCTCAAGTGAAGGAGGCGCGAGG 1445
 QY 1441 CTCTAAACACAGGGAATTACACAGCAAGTGTGGATGTGTGAGTTTGGGCTGTCT 1500
 Db 1446 CTCTAAACACG---GTTACACAGCAAGTGTGGATGTGTGAGTTTGGGCTGTCT 1502
 QY 1501 GGGAGCTCTCTCATATGAGAGCGGCTCGTACCTTAAATGTCTACTGAAGAGTGTGG 1560
 Db 1503 GGGAGCTCTCTCATATGAGAGCGGCTCGTACCTTAAATGTCTACTGAAGAGTGTGG 1562
 QY 1561 AGGCGGTGAGAGAGGGGTACCGCATGGAACCCCGGAGGGGTGTCCAGGCGCGGTGACG 1620
 Db 1563 AGGCGGTGAGAGAGGGGTACCGCATGGAACCCCGGAGGGGTGTCCAGGCGCGGTGACG 1622
 QY 1621 TCCTATGAGACAGCTGTGGAGAGAGAGCCCGCGCGGACCTTCCGCAAACTGG 1680
 Db 1623 TCCTATGAGACAGCTGTGGAGAGAGAGCCCGCGCGGACCTTCCGCAAACTGG 1681
 QY 1681 CCGAGAGCTGGCCCGGAGCTAGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1740
 Db 1682 CCGAGAGCTGGCCCGGAGCTAGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1741
 QY 1741 AGCGGAGGCTTCACCTCGCCCGCAAGCCAGAGCCCTGAGACCCAGCGGTGGGCGCT 1800
 Db 1742 AGCGGAGGCTTCACCTCGCCCGCAAGCCAGAGCCCTGAGACCCAGCGGTGGGCGCT 1800
 QY 1801 TGGCCCGAGAGAGAGAGAGAGTGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1860
 Db 1799 TGGCCCGAGAGAGAGAGAGAGTGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1858
 QY 1861 AGGTTCCAGGCGGCGAGTGTCTGTGTGTCGACAGAGAGGCGTGGCCAGCTAGAG 1920
 Db 1859 AGGTTCCAGGCGGCGAGTGTCTGTGTGTCGACAGAGAGGCGTGGCCAGCTAGAG 1918
 QY 1921 GGCTGTGGGCGGCGGTGTGAGACCCAGAGCTGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 1980
 Db 1919 GGCTGTGGGCGGCGGTGTGAGACCCAGAGCTGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 1978
 QY 1981 ATTCTAAG 1989
 Db 1979 ATTCTAAG 1987

RESULT 5
 US-09-315-928-1
 ; Sequence 1, Application us/09315928
 ; Patent No. 6368796
 ; GENERAL INFORMATION:
 ; APPLICANT: Avram, Jerome E.
 ; APPLICANT: Groopman, Jerome E.
 ; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
 ; FILE REFERENCE: MED97-01PAZ
 ; CURRENT FILING DATE: US/09/315, 928
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: US 08/876, 882
 ; PRIOR APPLICATION NUMBER: US 60/035, 228
 ; PRIOR FILING DATE: 1997-01-08
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1987
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (263) ... (1846)
 ; US-09-315-928-1

Query Match 95.5%; Score 1909.8; DB 4; Length 1987;
 Best Local Similarity 99.2%; Pred. No. 0;

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,989A
FILING DATE: February 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles E. Miller
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 1920-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1942 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: human
STRAIN: UT-7
US-08-604-989A-11

Query Match 95.2%; Score 1903.4; DB 2; Length 1942;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1939; Conservative 0; Mismatches 1; Indels 5; Gaps 3;

52 CGGAGGCGCTCTGGGGGGGGGGGGG--GGGGCTGGGGGGGGGGGGGGGAGAA 109
1 CGGAGGCGCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 60
110 CAGGAAGAACAGGCTCGGTCAGTGGACCCAGCTCCCTACTCTGTGGCAGCGCT 169
61 CAGGAAGAACAGGCTCGGTCAGTGGACCCAGCTCCCTACTCTGTGGCAGCGCT 120
170 GGCTGTGGCAGGCGATTCGCCAGCGTCCCGCACTGTGACACACTTGTCTGCTCTC 229
121 GGCTGTGGCAGGCGATTCGCCAGCGTCCCGCACTGTGACACACTTGTCTGCTCTC 180
220 ACCTGCGTCAGTTTCCCTCTGGGGGGGATGGGGGGGGGGGGGGGGTTCGTTTCTG 289
181 ACCTGCGTCAGTTTCCCTCT--GGGGGGGATGGGGGGGGGGGGGGTTCGTTTCTG 239
290 GGCAATTCACGCGTGTGATCTGTGTGAGAACTTCCCGGGGTGAGACCCCGGTTCTCG 349
240 GGCAATTCACGCGTGTGATCTGTGTGAGAACTTCCCGGGGTGAGACCCCGGTTCTCG 299
350 AGCTGGACCCCGCTCCCGTCTCAGCCAGATGCGCAAGAGGCGTGGGCCCGGCGAC 409
300 AGCTGGACCCCGCTCCCGTCTCAGCCAGATGCGCAAGAGGCGTGGGCCCGGCGAC 359
410 CCAAGTATCAACCAATGCGAGCAACCGCCCGCAAGGAGGAGGAGGAGGAGGAGGAG 469
360 CCAAGTATCAACCAATGCGAGCAACCGCCCGCAAGGAGGAGGAGGAGGAGGAGGAG 419
470 GGGGAGCTGTGATCATCTGAGAGCGCTGGAGAAAGAGCTGTACCGGTCAACGA 529
420 GGGGAGCTGTGATCATCTGAGAGCGCTGGAGAAAGAGCTGTACCGGTCAACGA 479

530 CCACACAGTGGACAGAGAGGGCTGTGGCACTGGGGGGGCTGGGGAGCGGGAGCCCT 589
480 CCACACAGTGGACAGAGAGGGCTGTGGCACTGGGGGGGCTGGGGAGCGGGAGCCCT 539
590 CTCCGAGAGCCCAAGCTCAGCTATGCGCGGTTCACAGGGAAGATCTCGGGCAGA 649
540 CTCCGAGAGCCCAAGCTCAGCTATGCGCGGTTCACAGGGAAGATCTCGGGCAGA 599
650 GGGTGTCAAGCAGCTGCAAGCTCCGAGAGTGGGCTGTCTGTGGGGAGTCCGCGG 709
600 GGGTGTCAAGCAGCTGCAAGCTCCGAGAGTGGGCTGTCTGTGGGGAGTCCGCGG 659
710 CCACCCCGGAGCTACGTCCTGTGGCTGAGCTTTGGCGCGGAGCATCTACCGGT 769
660 CCACCCCGGAGCTACGTCCTGTGGCTGAGCTTTGGCGCGGAGCATCTACCGGT 719
770 GCTGACCGGAGCGGAGCTACGTCCTGTGGCTGAGCTTTGGCGCGGAGCATCTAC 829
720 GCTGACCGGAGCGGAGCTACGTCCTGTGGCTGAGCTTTGGCGCGGAGCATCTAC 779
830 CATGGTGAAGCTTACAGCAAGAGGAGGCGCTATCTGCAACCAAGCTGTGAGACCAA 889
780 CATGGTGAAGCTTACAGCAAGAGGAGGCGCTATCTGCAACCAAGCTGTGAGACCAA 839
890 GCGGAACACAGGAGGAGGAGGCGCTGTGAGAGAGCTGGCGAGGGGGGCTGGTACTGA 949
840 GCGGAACACAGGAGGAGGAGGCGCTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAG 899
950 CCGTGAAGCTTACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1009
900 CCGTGAAGCTTACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 959
1010 GGGTGAAGCTTACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1069
960 GGGTGAAGCTTACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1019
1070 GGGCTTCTGAGCAGAGGAGGCGCTCATGACCAAGATGCAACAGCAAGCAAGCTGTCT 1129
1020 GGGCTTCTGAGCAGAGGAGGCGCTCATGACCAAGATGCAACAGCAAGCAAGCTGTCT 1079
1130 CCGTGAAGCTTACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1189
1080 CCGTGAAGCTTACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1139
1190 CCGTGAAGCTTACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1249
1140 CCGTGAAGCTTACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1199
1250 GTTTCTCTGACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1309
1200 GTTTCTCTGACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1259
1310 GAGCTGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1369
1260 GAGCTGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1319
1370 TGGCTGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1429
1320 TGGCTGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1379
1430 GGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1489
1380 GGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1439
1490 GGTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1549
1440 GGTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1499
1550 AGAGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1609
1500 AGAGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1559
1610 CCGCTGACAGCTCTCATGAGCAGCTGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1669

Db 1560 CCCCCGTCACGCTCCATCAGACAGCTGCTGGGAGGACAGCCCGCCCGGCGACCCCTT 1619
QY 1670 CCGCAACTGCGCCGGAAGCTGGCCCGGAGCTAGCGAGTGGCCCGACCCCTCCGT 1729
Db 1620 CCGCAACTGCGCCGGAAGCTGGCCCGGAGCTAGCGAGTGGCCCGACCCCTCCGT 1679
QY 1730 CTCAGGGCAGGACGCGGAGCTCCAGCTCCGCCCCGAGAGCCCTGACCCACC 1789
Db 1680 CTCAGGGCAGGACGCGGAGCTCCAGCTCCGCCCCGAGAGCCCTGACCCACC 1739
QY 1790 GGTGGGCGCTTGGCCCGGAGAGGACGAGAGTGGAGTGGCGGCTGGGGGCACTGAC 1849
Db 1740 GGT--GGCCCTTGGCCCGGAGAGGACGAGAGTGGAGTGGCGGCTGGGGGCACTGAC 1797
QY 1850 CAGGCCCAAGGAGGAGTCCAGGCGGGCAGTCACTCTCTGTCGCCACAGCGGGGCTGG 1909
Db 1798 CAGGCCCAAGGAGGAGTCCAGGCGGGCAGTCACTCTCTGTCGCCACAGCGGGGCTGG 1857
QY 1910 CCGACGTAGGGGCTCTGGGCGGCCCTGTGACACCCAGACCTCGGAAGGATGATCGCC 1969
Db 1858 CCGACGTAGGGGCTCTGGGCGGCCCTGTGACACCCAGACCTCGGAAGGATGATCGCC 1917
QY 1970 GATAAGACGATTTCTAAGACTCT 1994
Db 1918 GATAAGACGATTTCTAAGACTCT 1942

RESULT 7

US-08-604-989A-10

Sequence 10, Application US/08604989A

Patent No. 5834208

GENERAL INFORMATION:

APPLICANT: Sakano, S.

TITLE OF INVENTION: No. 5834208el Tyrosine kinase

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/604, 989A

FILING DATE: February 23, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Charles E. Miller

REGISTRATION NUMBER: 24,576

REFERENCE/DOCKET NUMBER: 1920-026

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1521 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE:

ORGANISM: human

STRAIN: UT-7

US-08-604-989A-10

Query Match

76.0%; Score 1519.4; DB 2; Length 1521;

Best Local Similarity 99.9%; Pred. No. 9,5e-300;
Matches 1520; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 258 ATGGGGGGGCGAGGCTCTCTGTTCTCTGCGGGGCAATTCACGCTGTGATTCCTGAG 317
Db 1 ATGGGGGGGCGAGGCTCTCTGTTCTCTGCGGGGCAATTCACGCTGTGATTCCTGAG 60
QY 318 GAACCTTCCCGGGGTAGGCCCCCGCTTCTCCGAGGCTGGACCCCCCTCCGCTCAGGC 377
Db 61 GAACCTTCCCGGGGTAGGCCCCCGCTTCTCCGAGGCTGGACCCCCCTCCGCTCAGGC 120
QY 378 AGGATGCCAACGAGGCGCTGGGCCCCGGGACCCAGTATCACCMAATGCGAGCACACC 437
Db 121 AGGATGCCAACGAGGCGCTGGGCCCCGGGACCCAGTATCACCMAATGCGAGCACACC 180
QY 438 CGCCCCAAGCCAGGGGAGCTGGCTTCCGCAAGGGCGAGCTGTGTAACCATCTCGAGGCC 497
Db 181 CGCCCCAAGCCAGGGGAGCTGGCTTCCGCAAGGGCGAGCTGTGTAACCATCTCGAGGCC 240
QY 498 TCGGAGAACAGAGCTGGTACCGCGCTCAAGACACACACAGTGGAGAGGAGGGGCTG 557
Db 241 TCGGAGAACAGAGCTGGTACCGCGCTCAAGACACACACAGTGGAGAGGAGGGGCTG 300
QY 558 GCAGCTGGGGGCGCTGCGGGAGCGGGAGGCCCTCTCCGAGAGACCCCAAGCTCAGCTCATG 617
Db 301 GCAGCTGGGGGCGCTGCGGGAGCGGGAGGCCCTCTCCGAGAGACCCCAAGCTCAGCTCATG 360
QY 618 CCGTGCTTCACAGGGGAGATCTCGGGGCCAGAGAGGCTGTCCAGCACTGACGCTCCGAG 677
Db 361 CCGTGCTTCACAGGGGAGATCTCGGGGCCAGAGAGGCTGTCCAGCACTGACGCTCCGAG 420
QY 678 GATGGGCTGTTCTGTTGCGGGAGTCCGCGGCCACCCCGGGGACTACGCTCTGTCGCG 737
Db 421 GATGGGCTGTTCTGTTGCGGGAGTCCGCGGCCACCCCGGGGACTACGCTCTGTCGCG 480
QY 738 AGCTTTGGCCGCGAGCTATCCATACCGCGTGTCTGACACCGGAGCGGCACCTCAATC 797
Db 481 AGCTTTGGCCGCGAGCTATCCATACCGCGTGTCTGACACCGGAGCGGCACCTCAATC 540
QY 798 GATGAGGCGCGTGTCTTCTGCAACCTCATGTGACATGTGTGAGCATTTACAGCAGACAG 857
Db 541 GATGAGGCGCGTGTCTTCTGCAACCTCATGTGACATGTGTGAGCATTTACAGCAGACAG 600
QY 858 GCGCTATCTGACCAAGCTGTGTGACCAAGCGGAACACGGGAGCCAGTCCGCGAG 917
Db 601 GCGCTATCTGACCAAGCTGTGTGACCAAGCGGAACACGGGAGCCAGTCCGCGAG 660
QY 918 GAGGAGCTGGCCAGGGCGGGCTGTTACTGAACTGCAAGCATTTGACATTTGGAGCACAG 977
Db 661 GAGGAGCTGGCCAGGGCGGGCTGTTACTGAACTGCAAGCATTTGACATTTGGAGCACAG 720
QY 978 ATCGGAGAGGAGAGATTTGGAGCTTCTGCAAGGGGTGAGTACCTGGGGCAAAAGTGGCC 1037
Db 721 ATCGGAGAGGAGAGATTTGGAGCTTCTGCAAGGGGTGAGTACCTGGGGCAAAAGTGGCC 780
QY 1038 GTGAAGATATCAATGTGATGTGACAGCCCGAGCTTCTGAGAGAGAGCGGCTCATG 1097
Db 781 GTGAAGATATCAATGTGATGTGACAGCCCGAGCTTCTGAGAGAGAGCGGCTCATG 840
QY 841 ACGAAGATGCAACAGAGAACCTGTGGGTCTCTGGGCGTATCTCGACACAGGGGCTG 900
Db 1098 ACGAAGATGCAACAGAGAACCTGTGGGTCTCTGGGCGTATCTCGACACAGGGGCTG 1157
QY 1158 TACATTGTGATGAGACAGCTGAGCAAGGCAACCTGTGTAATTTCTGCGGACCGGGGT 1217
Db 901 TACATTGTGATGAGACAGCTGAGCAAGGCAACCTGTGTAATTTCTGCGGACCGGGGT 960
QY 1218 CGAGCCCTGTGAACACCGCTCAGCTCTGCAAGTTTCTGACAGTGGCGGAGGGCATG 1277
Db 961 CGAGCCCTGTGAACACCGCTCAGCTCTGCAAGTTTCTGACAGTGGCGGAGGGCATG 1020
QY 1278 GAGTACTGTGAGAGCAAGACTTGTGACCGCGACCTGGCGCCCGCAACATCTGTGCTC 1337
Db 1337 GAGTACTGTGAGAGCAAGACTTGTGACCGCGACCTGGCGCCCGCAACATCTGTGCTC

Db 1021 GAGTACCTGAGAGCAAGAGCTTGTGCAACCGGACCTGGCCGCCGCAACATCTGTGTC 1080
 QY 1338 TCAGAGAGACCTGTGGGCAAGGTCAAGCACTTTGGCTGGCCAAAGCCGAGGGAAGGG 1397
 Db 1081 TCAGAGAGACCTGTGGGCAAGGTCAAGCACTTTGGCTGGCCAAAGCCGAGGGAAGGG 1140
 QY 1398 CTAGACTCAAGCCGGCTGCGCCGTCAAGGTGACGGCCCGGAGGCTCTCAAAACAGGGGAAG 1457
 Db 1141 CTAGACTCAAGCCGGCTGCGCCGTCAAGGTGACGGCCCGGAGGCTCTCAAAACAGGGGAAG 1200
 QY 1458 TTCACAGCAAGCGGATGTCTGAGACTTTGGGCTCTCTCTGAGAGGCTCTCTCATATAT 1517
 Db 1201 TTCACAGCAAGCGGATGTCTGAGACTTTGGGCTCTCTCTGAGAGGCTCTCTCATATAT 1260
 QY 1518 GGAAGGGCTCCGTACCTAAATGTCTCACTGAAAGAGTGTGAGAGCCGCTGAGAGAGGG 1577
 Db 1261 GGAAGGGCTCCGTACCTAAATGTCTCACTGAAAGAGTGTGAGAGCCGCTGAGAGAGGG 1320
 QY 1578 TACCGCATGAAACCCCGGAGGGCTGTCCAGAGCCCGCTGACGCTCTCATGAGCACTGC 1637
 Db 1321 TACCGCATGAAACCCCGGAGGGCTGTCCAGAGCCCGCTGACGCTCTCATGAGCACTGC 1380
 QY 1638 TGGGAGGCAAGCGCCGCGCGCCGACCCCTTCCGAAACTGGCCGAGAAAGTGGGCGCG 1697
 Db 1381 TGGGAGGCAAGCGCCGCGCGCCGACCCCTTCCGAAACTGGCCGAGAAAGTGGGCGCG 1440
 QY 1698 GAGCTACGAGTGCAGAGTGCAGGCTCCGCTCTCAGGCGAGGACGCGCAGGCTCCACC 1757
 Db 1441 GAGCTACGAGTGCAGAGTGCAGGCTCCGCTCTCAGGCGAGGACGCGCAGGCTCCACC 1500
 QY 1758 TGGCCCCGAAGCCAGGAGCC 1778
 Db 1501 TGGCCCCGAAGCCAGGAGCC 1521

; MOLECULE TYPE: cDNA to mRNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: human
 ; STRAIN: UT-7
 ; US-08-604-989A-9
 Query Match 69.9%; Score 1398; DB 2; Length 1398;
 Best Local Similarity 100.0%; Pred. No. 4e-275;
 Matches 1398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 ATGCCAAGAGCGCGCGCGCCCGGCGACCCAGTATATACCAAAATGCGAGCAGCACC 440
 Db 1 ATGCCAAGAGCGCGCGCGCCCGGCGACCCAGTATATACCAAAATGCGAGCAGCACC 60
 QY 441 CCCAAGCCAGGAGGAGCTGAGCTTCCGCAAGGGGAGAGTGTGACATCTCTGAGGCGCTGC 500
 Db 61 CCCAAGCCAGGAGGAGCTGAGCTTCCGCAAGGGGAGAGTGTGACATCTCTGAGGCGCTGC 120
 QY 501 GAGAACAGAGCTGTATACCGCTCAAGACACACACAGTGTGAGAGAGGAGGCTGTGCA 560
 Db 121 GAGAACAGAGCTGTATACCGCTCAAGACACACAGTGTGAGAGAGGAGGCTGTGCA 180
 QY 561 GCTGGGGGCGCTGGGGAGGGAGGGGCGCTCTCCGAGACCCCAAGCTCAGCCTCATGGCG 620
 Db 181 GCTGGGGGCGCTGGGGAGGGAGGGGCGCTCTCCGAGACCCCAAGCTCAGCCTCATGGCG 240
 QY 621 TGGTTCACGAGGAAATCTCGGGCCAGAGAGGCTGTCCAGCAGCTGCAAGCTCCCGAGAT 680
 Db 241 TGGTTCACGAGGAAATCTCGGGCCAGAGAGGCTGTCCAGCAGCTGCAAGCTCCCGAGAT 300
 QY 681 GGGCTGTCTCTGCTGGGAGTCCGGCGCCACCCCGGAGCTACGCTCTGTGCTGAGC 740
 Db 301 GGGCTGTCTCTGCTGGGAGTCCGGCGCCACCCCGGAGCTACGCTCTGTGCTGAGC 360
 QY 741 TTTGGCGGAGGAGTCACTACCTACGCGGTGTCTGACCGGAGGCGCCACCTCAATGAT 800
 Db 361 TTTGGCGGAGGAGTCACTACCTACGCGGTGTCTGACCGGAGGCGCCACCTCAATGAT 420
 QY 801 GAGGCGGTCTTCTTCTGCAACCTCATGAGATGAGTGTGAGCATTTACAGCAAGGCAAGGCG 860
 Db 421 GAGGCGGTCTTCTTCTGCAACCTCATGAGATGAGTGTGAGCATTTACAGCAAGGCAAGGCG 480
 QY 861 GCTATCTGCACCAAGCTGTGTGAGACCAAAAGCGGCAACAGGCAAGTCCCGGAGAG 920
 Db 481 GCTATCTGCACCAAGCTGTGTGAGACCAAAAGCGGCAACAGGCAAGTCCCGGAGAG 540
 QY 921 GAGCTGGCAGGCGGGGCTGTACTGAACTGACATTTGACATTTGGGAGCAGATC 980
 Db 541 GAGCTGGCAGGCGGGGCTGTACTGAACTGACATTTGACATTTGGGAGCAGATC 600
 QY 981 GGAAGGAGAGTTTGGAGCTGTCTGCAAGGGTGAATACCTGGGCGCAAAAGTGGCCGTG 1040
 Db 601 GGAAGGAGAGTTTGGAGCTGTCTGCAAGGGTGAATACCTGGGCGCAAAAGTGGCCGTG 660
 QY 1041 AAGATATCAAGTGTATGTGACAGCCAGGCTTCTTGGAGAGAGGCGGCTCATGAG 1100
 Db 661 AAGATATCAAGTGTATGTGACAGCCAGGCTTCTTGGAGAGAGGCGGCTCATGAG 720
 QY 1101 AAGATCAACAGAGAACCGGAGTGTCTGAGGCGTGTCTGACAGGAGGCTGTAC 1160
 Db 721 AAGATCAACAGAGAACCGGAGTGTCTGAGGCGTGTCTGACAGGAGGCTGTAC 780
 QY 1161 ATTGTATGAGAGCAGTGAAGCAAGGCAACCTGTGTAATTTCTGGGAGCCCGGCTGCA 1220
 Db 781 ATTGTATGAGAGCAGTGAAGCAAGGCAACCTGTGTAATTTCTGGGAGCCCGGCTGCA 840
 QY 1221 GCCCTGTGAACACCGCTCAAGCTCTGCAAGTTTCTCTGACAGTGGCCGAGGCAATGAG 1280
 Db 841 GCCCTGTGAACACCGCTCAAGCTCTGCAAGTTTCTCTGACAGTGGCCGAGGCAATGAG 900
 QY 1281 TACCTGAGAGCAAGAGCTGTGCAACCGGAGCCTGGCGCCGCAAACTCTGTGCTCA 1340
 Db 901 TACCTGAGAGCAAGAGCTGTGCAACCGGAGCCTGGCGCCGCAAACTCTGTGCTCA 960

QY 1928 GCGGCGCCCTGACACCCCGAGACCTGCGAAGATGATCCCGCATTAAGACGATTCTAA 1987
 Db 1617 GCGGCGCCCTGACACCCCGAGACCTGCGAAGATGATCCCGCATTAAGACGATTCTAA 1676
 QY 1988 GGACTCTAAATAA 2000
 Db 1677 GGAAAAAAAAAAAA 1689

RESULT 10
 US-08-604-989A-8
 : Sequence 8, Application US/08604989A
 : Patent No. 5834208
 : GENERAL INFORMATION:
 : APPLICANT: Sakano, S.
 : TITLE OF INVENTION: No. 5834208e1 Tyrosine Kinase
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pennie & Edmonds LLP
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10036-2711
 : COMPUTER READABLE FORM:
 : MEDIA TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FastSeq Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/604,989A
 : FILING DATE: February 23, 1996
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Charles E. Miller
 : REGISTRATION NUMBER: 24,576
 : REFERENCE/DOCKET NUMBER: 1920-026
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 790-9090
 : TELEFAX: (212) 869-8864/9741
 : TELEX: 66141 PENNIE
 : INFORMATION FOR SEQ ID NO: 8:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 738 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA to mRNA
 : ORIGINAL SOURCE:
 : ORGANISM: human
 : STRAIN: UT-7
 : US-08-604-989A-8

Query Match 36.9%; Score 738; DB 2; Length 738;
 Best Local Similarity 100.0%; Pred. No. 3e-141;
 Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 954 CAGCATTTGACATTTGGAGACAGATCGAGAGAGAGATTGAGCTGCTCGAGGCT 1013
 Db 1 CAGCATTTGACATTTGGAGACAGATCGAGAGAGAGATTGAGCTGCTCGAGGCT 60
 QY 1014 GAGTACCTGGGCAAAAGGTGGCCGTGAAGATATCAAGTGTGATGTGACAGCCAGGCC 1073
 Db 61 GAGTACCTGGGCAAAAGGTGGCCGTGAAGATATCAAGTGTGATGTGACAGCCAGGCC 120
 QY 1074 TTCCGAGAGAGAGAGCCGCTCATGACGAAGATGCAACAGCAAACTGGTGGCTCTCG 1133
 Db 121 TTCCGAGAGAGAGAGCCGCTCATGACGAAGATGCAACAGCAAACTGGTGGCTCTCG 180
 QY 1134 GGCCTGATCTGACACAGAGGCGCTGTACATTTGTCTATGAGACAGCTGAGCAAGGGCAACCTG 1193
 Db 181 GGCCTGATCTGACACAGAGGCGCTGTACATTTGTCTATGAGACAGCTGAGCAAGGGCAACCTG 240

QY 1194 GTGAACCTTCTGCGGACCCGCGGCTGAGCCCTCTGTGTAACACCGCTCAGCTCTGACATT 1253
 Db 241 GTGAACCTTCTGCGGACCCGCGGCTGAGCCCTCTGTGTAACACCGCTCAGCTCTGACATT 300
 QY 1254 TCTCTGACAGTGGCGGAGGAGCATGAGTACCTGTGAGAGCAAGAGCTTGTGACACCGGAC 1313
 Db 301 TCTCTGACAGTGGCGGAGGAGCATGAGTACCTGTGAGAGCAAGAGCTTGTGACACCGGAC 360
 QY 1314 CTGGCCCGCCGCAACATCTGCTGTGAGAGACCTGTGGCCAAAGGTCAGCCACTTTGGC 1373
 Db 361 CTGGCCCGCCGCAACATCTGCTGTGAGAGACCTGTGGCCAAAGGTCAGCCACTTTGGC 420
 QY 1374 CTGGCCCAAGCCGAGCGGAGGAGGCTAGACTCAAGCCGCTGCTCAAGTGAGACGCG 1433
 Db 421 CTGGCCCAAGCCGAGCGGAGGAGGCTAGACTCAAGCCGCTGCTCAAGTGAGACGCG 480
 QY 1434 CCGAGGCTCTCAACACGAGGAAGTTCACACAGCAAGTGGATGTGTGAGTTTGGGCTG 1493
 Db 481 CCGAGGCTCTCAACACGAGGAAGTTCACACAGCAAGTGGATGTGTGAGTTTGGGCTG 540
 QY 1494 CTGCTCTGGAGGCTTCTCATATGAGACGCGGCTCCGTAAATGTCACTGAAGAAG 1553
 Db 541 CTGCTCTGGAGGCTTCTCATATGAGACGCGGCTCCGTAAATGTCACTGAAGAAG 600
 QY 1554 GTGTGAGAGCCGTGAGAGAGGTAACCGCATGAAACCCCGAGGCGTGTCCAGGCC 1613
 Db 601 GTGTGAGAGCCGTGAGAGAGGTAACCGCATGAAACCCCGAGGCGTGTCCAGGCC 660
 QY 1614 GTGCACGTCTCATATGAGCAAGCTGTGGAGGAGACCCCGCGGCGCACCTTCCG 1673
 Db 661 GTGCACGTCTCATATGAGCAAGCTGTGGAGGAGACCCCGCGGCGCACCTTCCG 720
 QY 1674 AAACGTGCGCGAGAGCTG 1691
 Db 721 AAACGTGCGCGAGAGCTG 738

RESULT 11
 US-09-741-154-3
 : Sequence 3, Application US/09741154
 : Patent No. 6437110
 : GENERAL INFORMATION:
 : APPLICANT: BEASLEY, Ellen M. et al
 : TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 : TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 : FILE REFERENCE: C1001061
 : CURRENT APPLICATION NUMBER: US/09/741,154
 : CURRENT FILING DATE: 2000-12-21
 : NUMBER OF SEQ ID NOS: 4
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 3
 : LENGTH: 16389
 : TYPE: DNA
 : ORGANISM: Human
 : US-09-741-154-3

Query Match 22.8%; Score 455; DB 4; Length 16389;
 Best Local Similarity 100.0%; Pred. No. 1.3e-83;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1541 GTCACTGAAAGAGGTGTGAGAGCCGTGAGAGAGGAGTACCGCATGGAACCCCGAGGG 1600
 Db 13941 GTCACTGAAAGAGGTGTGAGAGCCGTGAGAGAGGAGTACCGCATGGAACCCCGAGGG 14000
 QY 1601 CTGTCCAGAGCCCGGTGACAGTCTCATAGACAGCTGTGTGGAGGAGAGCCCGCCGCG 1660
 Db 14001 CTGTCCAGAGCCCGGTGACAGTCTCATAGACAGCTGTGTGGAGGAGAGCCCGCCGCG 14060
 QY 1661 GCCACCTTCGCAAACTGAGGCGGAGAGGCTGGCCGCGGAGCTAGCAGTGCAGTGGCC 1720
 Db 14061 GCCACCTTCGCAAACTGAGGCGGAGAGGCTGGCCGCGGAGCTAGCAGTGCAGTGGCC 14120

Query Match	10.0%;	Score 199.2;	DB 1;	Length 1602;
Best Local Similarity	-55.7%;	Pred. No. 7.2e-32;		
Matches 453; Conservative	0;	Mismatches 343;	Indels 18;	Gaps 3;

QY	897	IACGGACCAAGTGGGCGGAGAGAGAGTGGCCAGGGCGGGCTGTACTGAACTCCAG	956
Db	736	CCACGTCACAGCCCGACAGACCAGAGACTGCCCAAGGACGGGTGGAAATCCCCGGGAG	795
QY	957	CATTGACATTTGGGAGCACAGATCGAGAGGGAGGATTTGAGAGCTGTCTGACAGG--T	1013
Db	796	TCGCTGGGGGTGGAGGTGAAGCTGGGGCAGGGCTTTGGAGAGGTCGTGATGGGAGCC	855
QY	1014	GAGTAACTGGGGCAAAAGGTGGCCGTAAAGAAATTCAG--TGTGATGTGACAGCCAG	1070
Db	856	TGGAACGGCAACACCAAGATGGCCATTAAGACTCTGAAAGCCCGGCAACATGTCCCGGAG	915
QY	1071	GCCCTTCGTGGACGAGGGCGTCATACGCAAGATGGCAACAGCAAGAACTGGTGGCTC	1130
Db	916	GCCCTTCGTGGACGAGGGCGTCATACGCAAGATGGCAACAGCAAGAACTGGTGGCTC	975
QY	1131	CTGGGCGCTGATCTCTGACACAGGGGCTGTACATTTCTCATGAGCACGTGAGCAAGGGCAAC	1190
Db	976	TACGCACTGGGTGGAAAGACCCTATCTCATGCTACTGTGATCATGAGCAAGGGGAGC	1035
QY	1191	CTGGTGAACTTTCTGGCGGACCCGGGGTTCGAGCCCTCGTGAACACCCTCAGCTCTCGAG	1250
Db	1036	CTCCTGGATTTCTGAAAGGGAGAGATGGGCAAGTACTGCGGCTGCCACAGCTGTGCGAT	1095
QY	1251	TTTTCTCTGACAGTGGCCGAGAGGCTGATGAGTACTGTGAGACAGAACTTGTACCCGC	1310
Db	1096	ATGGCTCTCAGATTTGATCGCGCATGGCCATGTGGAGAGATGAACTACGTACACGGA	1155
QY	1311	GACCTGGCCGCGGCAACATCTGTGTTCTAGAGAGACTGTGGCCAAAGTCAAGCGACTTT	1370
Db	1156	GACCTGGGGCGGGCAACATCTGTGTTGGGGAGAACTGGTGTGTCAGAGTGGGCTGACTTT	1215
QY	1371	GGCCTGGCCAAAGCGGAGGGGCTGAGCTCAAGCCGGC-----TGGCC	1418
Db	1216	GGGCTGGCACGGCTCATTCGAGAGACACGAGTACACACAGCGGCAAGGTGCCAAGTCCCC	1275
QY	1419	GTCAAAGTGAAGCGGCGCCGAGGCGTCTCAAAACACGGGAAATTACACAGACAGTCCGATGC	1478
Db	1276	ATCAAGTGAAGAGGCGCCGAGGAGCGCCCTCATGTGGCGGTTACACATCAAGTGGGATGTC	1335
QY	1479	TGCAAGTTTGGGGTGTCTCTGTGGAGGCTTCTCATATGAGACGGGCTCCGTACCTTAAA	1538
Db	1336	TGGTCTTCGGCAATCTCTGTGACTGAGACTGACCCACCAAGGGCCGGGTGCATATCCCAAGG	1395
QY	1539	ATGTCACATGAAAGAGTGTGGGAGGCGGTGGAGAGAGGGGTATCCCATGGAACCCCGGAG	1598
Db	1396	ATGGTCAACAGGGAGGTGTCTGTGACACAGGTGAGAGGGGGCTTACCCCATATGCCCTGCCGCC	1455
QY	1599	GCGTGTCCAGGCCCGTGTGACAGTTCATGAGCAAGCTGTGGAGGAGCAAGCCCGCCGC	1658
Db	1456	GAGTGGCCCAAGTGTGCTGATGACTCATGTGCGCAAGTGTGGCGGAGGAGACCTGAGAG	1515
QY	1659	CGGCAACCTTCCGCAAACTGGCGGAAGACTGG	1692
Db	1516	CGGCGCACTTTTGATGACTGCAAGGCGCTTCTGG	1549

Search completed: September 13, 2003, 02:44:47
Job time : 147 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 13, 2003, 02:41:26 ; Search time 99 Seconds
(without alignments)
2260.417 Million cell updates/sec

Title: US-09-977-260-2
Perfect score: 2671
Sequence: 1 MAGRGLVWRAFHGCDNAE.....PASVSGQDADGSTRPSRQEP 507

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 segs, 220691566 residues
Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xip
-Q=/cgn2_1/USPTO.spool_p/US09977260/runat_11092003.141236.18221/app.query.fasta.1.647
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=trn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosun62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptlo -NORM=ext -HEAPSIZE=500 -MTLEN=0 -MAXLEN=2000000000
-USPR=US09977260.cgn2_1.1.85.tunat_11092003.141236.18221 -NCP=6 -ICP=3
-NO_MMAP -IAREQUERY -NEG_SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2671	100.0	1942	2	US-08-604-989A-11
2	2671	100.0	2000	4	US-08-426-509A-1
3	2671	100.0	2000	4	US-08-232-545-1
4	2671	100.0	2000	5	PCT-US95-05008-1
5	2662	99.7	1521	2	US-08-604-989A-10
6	2591.5	97.0	1987	2	US-08-876-882-1
7	2591.5	97.0	1987	4	US-09-315-928-1
8	2444	91.5	1398	2	US-08-604-989A-9
9	2020.5	75.6	1713	4	US-09-741-154-1
10	1469.5	55.0	16389	4	US-09-741-154-3
11	1269	47.5	738	2	US-08-604-989A-8
12	737.5	27.6	1602	1	US-07-820-011A-1

13	737.5	27.6	1602	5	PCT-US93-00445-1	Sequence 1, Appl
14	727	27.2	1611	1	US-07-820-011A-3	Sequence 3, Appl
15	727	27.2	1611	5	PCT-US93-00445-3	Sequence 3, Appl
16	727	27.2	2129	4	US-09-016-434-1452	Sequence 1452, Ap
17	710	26.6	4517	5	PCT-US93-06251-83	Sequence 83, Appl
18	702.5	26.3	2647	4	US-09-220-132-77	Sequence 77, Appl
19	702.5	26.3	2647	5	PCT-US93-06251-77	Sequence 1, Appl
20	691.5	25.9	1491	2	US-09-006-675-1	Sequence 1, Appl
21	691.5	25.9	1491	3	US-09-228-603A-1	Sequence 35, Appl
22	683.5	25.6	3623	1	US-08-306-691B-35	Sequence 2, Appl
23	680	25.5	1467	4	US-09-579-182-2	Sequence 1, Appl
24	680	25.5	1548	4	US-09-099-053-1	Sequence 1, Appl
25	656	24.6	2827	4	US-08-492-723-1	Sequence 5, Appl
26	654.5	24.5	2770	4	US-08-426-509A-5	Sequence 5, Appl
27	654.5	24.5	2770	4	US-08-232-545-5	Sequence 5, Appl
28	654.5	24.5	2770	5	PCT-US95-05008-5	Sequence 5, Appl
29	654.5	24.5	7607	1	US-08-222-616-19	Sequence 19, Appl
30	654.5	24.5	7607	4	US-08-446-648-19	Sequence 19, Appl
31	654.5	24.5	7607	5	PCT-US95-04228-19	Sequence 1, Appl
32	608.5	22.8	2674	4	US-09-817-180-1	Sequence 1, Appl
33	607	22.7	2505	1	US-08-391-615-1	Sequence 1, Appl
34	595.5	22.3	3503	1	US-07-631-717A-1	Sequence 1, Appl
35	595.5	22.3	3503	1	US-08-166-717D-1	Sequence 1, Appl
36	591	22.1	1875	1	US-08-070-165F-3	Sequence 3, Appl
37	591	22.1	1875	2	US-08-885-418-3	Sequence 3, Appl
38	587	22.0	2456	4	US-09-016-434-1476	Sequence 1476, Ap
39	587	22.0	2500	4	US-08-426-509A-3	Sequence 3, Appl
40	587	22.0	2500	4	US-08-232-545-3	Sequence 3, Appl
41	587	22.0	2500	5	PCT-US95-05008-3	Sequence 3, Appl
42	582	21.8	2049	4	US-09-099-749-10	Sequence 10, Appl
43	581.5	21.8	5993	3	US-09-383-630-1	Sequence 1, Appl
44	581.5	21.8	5993	3	US-09-383-630-2	Sequence 2, Appl
45	576.5	21.6	2469	1	US-07-997-133-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-604-989A-11
Sequence 11 Application US/08604989A
Patent No. 5834208
GENERAL INFORMATION:
APPLICANT: Sakano, S.
TITLE OF INVENTION: No. 5834208el Tyrosine Kinase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennile & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,989A
FILING DATE: February 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles E. Miller
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 1920-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1942 base pairs
TYPE: nucleic acid

```

;
; STRANDEDNESS: double
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA to mRNA
;
; ORIGINAL SOURCE:
;
; ORGANISM: human
;
; STRAIN: UT-7
;
; US-08-604-989A-11

Alignment Scores:
Pred. No.: 2,176-257 Length: 1942
Score: 2671.00 Matches: 507
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-977-260-2 (1-507) x US-08-604-989A-11 (1-1942)

QY 1 MetAlaGlyArgGlySerLeuValSerTrpArgAlaPheHisGlyCysAspSerAlaGlu 20
DB 208 ATGGGGGGGCGAGGCTCTGTGGTTCTGGCGGGCATTTTCACAGGCTGTGATTCCTGCTGAG 267
QY 21 GluLeuProArgValSerProArgPheLeuArgAlaTrpHisProProValSerAla 40
DB 268 GAACCTCCCGGGGTAGGCCCGCCGCTTCTCCGAGCCTGGACCCCGCTCCCTCAGCC 327
QY 41 ArgMetProThrArgArgTrpAlaProGlyThrGlnCysIleThrLysCysGluHisThr 60
DB 328 AGGATGCCCAAGAGCGCTGGGGCCCGGGCACCCAGTGTATCACAATGCGAGCACACC 387
QY 61 ArgProLysProGlyGluLeuAlaPheArgLysGlyAspValValThrIleLeuGluAla 80
DB 388 CGCCCAAGCCAGGGGAGCTGGCTTCGCGAAGGGCGAGCTGTACACATCCTGGAGGCC 447
QY 81 CysGluAsnLysSerTrpTrpArgValLysHisIleThrSerGlyGlnGluLeuLeu 100
DB 448 TGGGAGAACAGAGCTGGTACCGGCTCAAGCACACACAGTGGAGAGGGGCTGCTG 507
QY 101 AlaAlaGlyAlaLeuArgGluArgGluAlaLeuSerAlaAspProLysLeuSerLeuMet 120
DB 508 GCAGCTGGGGCGCTCGGGAGCGGAGGCCCTCTCCGAGACCCCAAGCTCAGCTCATG 567
QY 121 ProTrpPheHisGlyLysIleSerGlyGlnGluAlaValGlnGlnLeuGlnProProGlu 140
DB 568 CCGTGGTTCCACGGGAAATCTCGGGCCAGAGGCTGTCCACAGCTCGAGCTCCGAG 627
QY 141 AspGlyLeuPheLeuValArgGluSerAlaArgHisProGlyAspTyrValLeuGlyVal 160
DB 628 GATGGGCTGTCTCGTGGGGAGTCCGCCGCCACCCCGGCGACTAGCTCTGTGCTG 687
QY 161 SerPheGlyArgAspValIleHisTyrArgValLeuHisArgAspGlyHisLeuThrIle 180
DB 688 AGCTTTGGCGCGGAGCTATCCATCACCGCGTGCACCGGAGCGGCACCTCATCATC 747
QY 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValGlnHisTyrSerLysAspLys 200
DB 748 GATGAGGCGCGTGTCTTCTGCACACCTCATGACATGGAGGAGTGAACATTAAGCAAG 807
QY 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGlu 220
DB 808 GGGCTATCTCGACCAACCTGTGTAGACCAAAAGCGGAAACAGGAGCAAGTCCGCCG 867
QY 221 GluGluLeuAlaArgAlaGlyLysTrpLeuLeuAsnLeuGlnHisLeuThrLeuGlyAlaGln 240
DB 868 GAGGAGCTGGCCAGCGGCGCGCTGTACTGAACCTGCAGCATTTTGAATTGGAGCACAG 927
QY 241 IleGlyGluGlyGluPheGlyAlaValLeuGlnGlyLysTyrLeuGlyGlnLysValAla 260
DB 928 ATCGGAGAGGAGAGACTTTGGAGCTGTCTCGCAGGCTGAGTACTCTGGCAAAAGGTGCC 987
QY 261 ValLysAsnIleLysCysAspValThrAlaGlnAlaPheLeuAspGlyThrAlaValMet 280
DB 988 GTGAAGAATATCAAGTGTGATGTGACAGCCCAAGGCTTCTGTGACGAGAGCGGCTCATG 1047

```

```

QY 281 ThrLysMetGlnHisGluAsnLeuValArgLeuLeuGlyValIleLeuHisGlnGlyLeu 300
DB 1048 ACGAAGATGCACACAGAGAACTGGCTGCTCTCTGGGCTGATGCTGCACAGGAGGCTG 1107
QY 301 TyrIleValMetGlnHisValSerLysGlyAsnLeuValAspPheLeuArgThrArgGly 320
DB 1108 TACATTGTATGACACAGTGTAGCAAGGGCAACCTGTGTAACTTTCTGTGGGACCGGGGT 1167
QY 321 ArgAlaLeuValAsnThrAlaGlnLeuLeuGlnPheSerLeuHisValAlaGluGlyMet 340
DB 1168 CGAGCGCTGTGTAAACACCGCTCAGCTCTCGCAGATTTCCTGTACAGTGGCCGAGGCAAG 1227
QY 341 GluTyrLeuGluSerLysLysLeuValHisArgAspLeuAlaAlaArgAsnIleLeuVal 360
DB 1228 GAGTACTGTGAGAGCAAGAACTTGTGCACCCGCACTGGCCCGCCGCAACCTCTGCTG 1287
QY 361 SerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGluArgLysGly 380
DB 1288 TCAGAGGAGCTGTGTGGCCAAAGGTCAAGCACTTTGGCTGTGGCCAAAGCCGAGGAGGG 1347
QY 381 LeuAspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLys 400
DB 1348 CTAGACTCAAGCCGCGCTGCCCTCAAGTGCAGCGGCCCGAGGCTCTCAAAACCGGAG 1407
QY 401 PheThrSerLysSerAspValTrpSerPheGlyValLeuLeuTrpGluValPheSerTyr 420
DB 1408 TTCACACAGCAAGTGTGAGTGTGTGGAGTTTGGGCTGTCTGTGGAGAGGTCTTCTCAT 1467
QY 421 GlyArgAlaProTyrProLysMetSerLeuLysGlyValSerGluAlaValGluLysGly 440
DB 1468 GGAGGGCTCTGTACCTTAAATGTCACTGAAAGAGGTTCGAGAGCCGTGGAGAAAGGG 1527
QY 441 TyrArgMetGluProProGluGluLysCysProGlyProValHisValLeuMetSerSerCys 460
DB 1528 TACCGCATGGAACCCCGGAGGCTGTCCAGGCCCGCTCAGCTCTATGACAGCTGC 1587
QY 461 TrpGluAlaGluProAlaArgArgProProPheArgLysLeuAlaGluLysLeuAlaArg 480
DB 1588 TGGGAGGCGAGACCCCGCCCGCCGACCTTCCGCAAACTGGCGAGAACTGGCCCG 1647
QY 481 GluLeuArgSerSerAlaGlyValAlaProAlaSerValSerGlyGlnAspAlaAspLysSerThr 500
DB 1648 GAGCTACGAGTGTGAGGTGCCCAAGCTCTCGTCAAGGAGAGAGCCGAGCGGCTCCAC 1707
QY 501 SerProArgSerGlnGluPro 507
DB 1708 TCGCCCGCAAGCCAGAGAGCC 1728

RESULT 2
US-08-426-509A-1
; Sequence 1, Application US/08426509A
; Patent No. 6326469
;
; GENERAL INFORMATION:
;
; APPLICANT: Ullrich, Axel
; APPLICANT: Gishlitzky, Mikhail
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; TITLE OF INVENTION: TYROSINE KINASES
; NUMBER OF SEQUENCES: 21
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York,
; STATE: NY
;
; COUNTRY: USA
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTA/Seq Version 2.0
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2000 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-426-509A-1

Alignment Scores:
Pred. No.: 2.27e-257 Length: 2000
Score: 2671.00 Matches: 507
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-977-260-2 (1-507) x US-08-426-509A-1 (1-2000)

QY 1 MetalaglyarvglyserleuvalsertrparqalaphhehsglycysaspsrAlaglu 20
DB 258 ATGGCGGGGGAGGCTCTGCTTCTGGGGGCAATTCAGGCTGTGATCTGGTGAG 317
QY 21 GluleuProarqyValSerProArqPheleuArqalatrPhIsProproProvalSerAla 40
DB 318 GAACCTCCCGGGGAGACCCCGGCTCTCCGAGCCGAGCCGCCCGCTCCGCTCAGGCC 377
QY 41 ArgmetProthrArqatgtrpAlaproglyThrIncysIlethrLysGluHisThr 60
DB 378 AGGATGGCAAGAGAGCCCTGGGCCCGGCAACCAGTGTATCACCAATGGAGCACACC 437
QY 61 ArgProLysProgluyluAlaPheArqLysGlyAspValIthrIleuGluAla 80
DB 438 CGCCCAAGCCAGGGGAGCTGGCTTCGCAAGGGGCACTGGTCAACATCTGGAGGCC 497
QY 81 CysGluAsnLysSerTrpTyArgValIlyshHisThrserGlyGlnGlyLeu 100
DB 498 TGGAGAAACAAGACTGTGACCGGCTCAGACCAACCAAGTGAAGAGGGCTGCTG 557
QY 101 AlAlaIyAlaLeuArqGluArqGluAlaLeuSerAlaAspProLysLeuSerLeuMet 120
DB 558 GCACCTGGGGCGCTGGCGGAGCGGAGGCCCTCTCCAGACCCCAAGCTCAGCTCATG 617
QY 121 ProtrPhehIsGlyLysIleSerGlyGlnGluAlaGlnGlnLeuInProProglu 140
DB 618 CCGGGGTCCAGGGGAAAGATCTCGGGCCAGAGGCTGTCCAGCACTGACCTCCCGAG 677
QY 141 AspIlyLeuPheLeuValArqGluSerAlaArqHisProgluYasPTrValLeuCysVal 160
DB 678 GATGGGCTGTTCGTGGTGGGAGTCCGGCGGCCACCCGGCGACTACGTCTGTGGTG 737
QY 161 SerheGlyArqAspValIleHisTyArqValLeuHisArqAspGlyHisLeuThrIle 180
DB 738 AGCTTTGGCGCGAGCTATCCACTACCGGTGCTGACCGCGAGCGGCACTCATCATC 797
QY 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValGluHisTySerLysAspLys 200
DB 798 GATGAGGCCGCTGTCTCTGCAACCTCATGATGATGGTGGAGCTTTCAGCAAGAGCAAG 857
QY 201 GlyAlaIleCysThrLysLeuValArqProLysArqLysHisGlyThrLysSerAlaGlu 220

DB 858 GGGCTATCTGCACCAAGCTGTGTGAGACCAAGGGAACAGGAGCAAGTCCGGCAG 917
QY 221 GluGluLeuAlaArqAlaGlyTrpLeuLeuAsnLeuGlnHisLeuThrLeuGlyAlaGln 240
DB 918 GAGAGCTGGCCAGGGGGGCTGTACTCAACCTGCAGCATTTGACATTTGGGAGCAG 977
QY 241 IleGlyGlnGlyGluPheGlyAlaValLeuGlnGlyGluTyrrLeuGlnGlyHisValAla 260
DB 978 ATCGAGAGAGGAGATTGGAGCTGTCTCTGACAGGCTAGTACTGGGGCAAAAGTGGCC 1037
QY 261 ValLysAsnIleLysCysAspValThrAlaGlnAlaPheLeuAspGluThrAlaValMet 280
DB 1038 GTGAAGAATATCAAGTGTGATGTGACAGCCAGGCTTCTCTGAGCAGAGAGCGCGTCATG 1097
QY 281 ThrLysMetGlnHisGluAsnLeuValArqLeuGlnGlyAlaIleLeuHisGlnGlyLeu 300
DB 1098 ACGAAGATGCACACGAGAACCTGGTCTCTCTGGCGGTGATCTGCACACAGGGGCTG 1157
QY 301 TyrIleValMetGluHisValSerLysGlyAsnLeuValAsnPheLeuArqThrArgGly 320
DB 1158 TACATTTCTATGGAGCACGTGAGCAAGGCAACCTGTGAACTTTCTGGAGACCCGGGCT 1217
QY 321 ArgAlaLeuValAsnThrAlaGlnLeuGlnPheSerLeuHisValAlaGlnGlyMet 340
DB 1218 CGAGCCCTCGTAACACCGGTCACGCTCGATGATTTCTCTGACGTCGGCGAGGCGCATG 1277
QY 341 GluTyrrLeuGlnSerLysLysLeuValHisArqAspLeuAlaAlaArqAsnIleLeuVal 360
DB 1278 GAGTACCTGAGAGCAAGACCTGTGTACCGGCAACCTGGCGGCCCAACATCTGTGTC 1337
QY 361 SerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGluArqLysGly 380
DB 1338 TCAGAGACCTCGTGGCCCAAGTCAAGCACTTTGGCTTGCCCAAGCCGAGCGGAAGGG 1397
QY 381 LeuAspSerSerArqLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLys 400
DB 1398 CTAGACTCAAGCCGGCTGCCGTCAGAGGAGCGCGCCGAGCTCTCAAAACAGCGGAAG 1457
QY 401 PheThrSerLysSerAspValItrpSerPheGlyValLeuLeuTrpGluValPheSerTyrr 420
DB 1458 TTCACAGCAAGTGGATGTGAGTTTGGGGTGTCTGCTGGAGGGTCTTCTCATAT 1517
QY 421 GlyArqAlaProTyrrProLysMetSerLeuLysGluValSerGluAlaValGluLysGly 440
DB 1518 GGAGGGCTCCGTACCTTAATATCTACTGAAGAAGTGTGGAGGCCGTGGAGAAGGG 1577
QY 441 TyrArgMetGluProProgluGlyCysProgluProValHisValLeuMetSerSerCys 460
DB 1578 TACCGCATGGAACCCCGGAGGGCTGTCCAGGCCCGGTCACGTCTCATAGCAGCTGC 1637
QY 461 TrpGluAlaGluProAlaArqArqProProPheArqLysLeuAlaGluLysLeuAlaArg 480
DB 1638 TGGGAGGACAGCCCGCGCGGCAACCTTCGCAAACTGGCGGAGAACTGGCCGG 1697
QY 481 GluLeuArqSerAlaGlyAlaProAlaSerValSerGlyGlnAspAlaAspGlySerThr 500
DB 1698 GAGCTAGCAAGTGCAGAGTGGCCCAAGCTCCGTCTCAGGGCAGAGCCGAGGCTCCACC 1757
QY 501 SerProArqSerGlnGluPro 507
DB 1758 TCGCCCGAAGCCAGAGGCC 1778

RESULT 3
US-08-232-545-1
Sequence 1, Application US/08232545
Patent No. 6506578
GENERAL INFORMATION:
APPLICANT: ulrich, Axel
APPLICANT: Gishitzky, Mikhail
APPLICANT: Sures, Irmann G.
TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2000 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-08-232-545-1
Alignment Scores:
Pred. No.: 2, 27e-257 Length: 2000
Score: 2671.00 Matches: 507
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-977-260-2 (1-507) x US-08-232-545-1 (1-2000)
QY 1 MetAlaGlyArgGlySerLeuValSerTrpArgAlaPheHisGlyCysAspSerAlaGlu 20
DB 258 ATGGGGGGGGGAGGCTCTGCTGTTCTCGCGGCAATTTCACGGCTGATTCGCTGAG 317
QY 21 GluLeuProArgValSerProArgPheLeuArgAlaTrpHisProProProValSerAla 40
DB 318 GAACCTCCCGGGGTAAGCCCGCTTCCTCCGAGCCTGGACCCCTCCCTCCGCTCAGCC 377
QY 41 ArgMetProThrArgArgTrpAlaProGlyThrGlnCysIleThrLysCysGlnHisThr 60
DB 378 AGGATGCCAAGAGGGGCGTGGGCCCCGGGCAACCAGTGTATGACCAAAAGCAGCACACC 437
QY 61 ArgProLysProGlyGluLeuAlaPheArgLysGlyAspValValThrIleLeuGluAla 80
DB 438 CCCCCCAAGCCAGGGGAGCTGGCTTCGCGAAGGGCGAGCTGGTCAACCATCTCGAGGCC 497
QY 81 CysGluAsnLysSerTrpTrpArgValLysHisHisThrSerGlyGlnGluLysLeu 100
DB 498 TCCGAGAACAGAGCTGGTACCGGCTCAAGCACACACACAGTGAAGAGGGGCTGCTG 557
QY 101 ATAAlaGlyAlaLeuArgGluArgGluAlaLeuSerAlaAspProLysLeuSerLeuMet 120
DB 558 GCAGCTGGGGGCTCGGGAGGAGGAGGAGGCTTCGCGAGACCCCAAGCTCAGCTCATG 617
QY 121 ProTrpPheHisGlyLysIleSerGlyGlnGluAlaValGlnGlnLeuGlnProProGlu 140
DB 618 CCGTGGTTCACAGGAGATCTCGGGGCGAGGAGCTGTCCACAGCTGACGCTCCCGAG 677
QY 141 AspGlyLeuPheLeuValArgGluSerAlaArgHisProGlyAspTyrValLeuCysVal 160

|||||
DB 678 GATGGGCTCTCTGGCGGGAGTCCGGCGCACCCGGGACATACCTCTGTCGGTG 737
QY 161 SerPheGlyArgAspValIleHisTrpArgValLeuHisArgAspGlyHisLeuThrIle 180
DB 738 AGCTTGGCGCGGACGCTCATCCACTACCGCGCTCTGACCGGACGCGCCACTCACAAAC 797
QY 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValGluHisTyrSerLysAspLys 200
DB 798 GATGAGCGCGTGTCTTCTGCAACCTCATGAGCATGTGGACATTAACAGAAAGCAAG 857
QY 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGlu 220
DB 858 GGGCTATGTGACCAAGCTGGTGAACCAAGGGAACGCGGAGCAAGTGGCGGAG 917
QY 221 GluGluLeuAlaArgAlaGlyTrpLeuLeuAsnLeuGlnHisLeuThrLeuGlyAlaGln 240
DB 918 GAGGAGCTGGCCAGGGCGGGGCTGTGATTGACMACTGACATTTTGACATTTGGAGGACAG 977
QY 241 IleGlyGluGlyGluPheGlyAlaValLeuGlnGlyGluTyrLeuGlyGlnLysValAla 260
DB 978 ATCGGAGAGGAGAGTTTGAGCTGTCTGCAAGGAGTACTGGGCGCAAAAGTGCGCC 1037
QY 261 ValLysAsnIleLysCysAspValIleThrAlaGlnAlaPheLeuAspGlyThrAlaValMet 280
DB 1038 GTGAAGAAATATCAAGTGTATGTGACAGCCAGGCTTCTGAGCAGAGCGGCTCATG 1097
QY 281 ThrLysMetGlnHisGluAsnLeuValArgLeuLeuGlyValIleLeuHisGlnGlyLeu 300
DB 1098 ACGAAGATGCACACAGCAAGAACTGTGGCTCTCTGCGGTATCTGACCAAGGGGCTG 1157
QY 301 TyrIleValMetGluHisValSerLysGlyAsnLeuValAsnPheLeuArgThrArgGly 320
DB 1158 TACATGTGTATGAGACACGTGAGCAAGGCGCAACCTGTGAACCTTCTCGCGACCGCGGCT 1217
QY 321 ArgAlaLeuValAsnThrAlaGlnLeuLeuGlnPheSerLeuHisValAlaGluGlyMet 340
DB 1218 CAGGCCCTGTGAACACCGCTCACTGCTGCAAGTTTCTCTGACCTGACCGCAAGGGCAG 1277
QY 341 GluTyrLeuGluSerLysLysLeuValHisArgAspLeuAlaAlaArgAsnIleLeuVal 360
DB 1278 GAGTACTGTGAGAGCAAGAGCTTGGCGACCCGCACTGGCGCGCGCAACATCTCGTGC 1337
QY 361 SerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGluArgLysGly 380
DB 1338 TCAGAGGAGACTGTGTGGCCAAAGTCAAGCACTTGGCTGCGCAAAAGCCGAGGAAAG 1397
QY 381 LeuAspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLys 400
DB 1398 CTGAGCTCAAGCCGGCTGCCCTCAAGTGGAGGCGCCCGAAGCTTCAAAACGGGAAG 1457
QY 401 PheThrSerLysSerAspValIlePhePheGlyValLeuLeuTrpGluValPheSerTyr 420
DB 1458 TTCACACAGCAAGTCCGATGTCTGAGATTGGGGTGGTCTCTGGGAGGCTTTCATAT 1517
QY 421 GlyArgAlaProTyrProLysMetSerLeuLysGluValSerGluAlaValGluLysGly 440
DB 1518 GCACGGGCTCCCTACCTTAATATGTACAGAAAGAGTGTCCGAGGCGCTGAGAAAGGG 1577
QY 441 TyrArgMetGluProProGluGlyCysProGlyProValHisValLeuMetSerCys 460
DB 1578 TACCGATGGAAACCCCGGAGGGCTGTCCAGGCCCCGCTGACGCTCTCTTGAGCAAGTGC 1637
QY 461 TrpGluAlaGluProAlaArgArgProPheArgLysLeuAlaGluLysLeuAlaArg 480
DB 1638 TGGAGGAGAGACCCGCGCGCGGACACCTTCCGCAAACTGGCGAAGAGCTGGCGCG 1697
QY 481 GluLeuArgSerAlaGlyAlaProAlaSerValSerGlyGlnAspAlaAspGlySerThr 500
DB 1698 GAGCTAACGAGTGCAGGTGGCCCAAGCTCCGTTCAAGGAGCAGAGCGGACGGCTCCACC 1757
QY 501 SerProArgSerGlnGluPro 507
|||||

Db 1758 TCGCCCCGAAGCCAGAGCCC 1778
RESULT 4
PCT-US95-05008-1
Sequence 1, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Wissenschaften E.V.
APPLICANT: Horigarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2000 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
PCT-US95-05008-1
Alignment Scores:
Pred. No.: 2,27e-257 Length: 2000
Score: 2671.00 Matches: 507
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-977-260-2 (1-507) x PCT-US95-05008-1 (1-2000)
QY 1 MetalGlyArgGlySerLeuValSerTPARAlaPheHisIscLysAspSerAlaGlu 20
Db 258 ATGGCGGGGGAGGCTCTCTGCTTCCTGGCGGGGCAATTCACGCTGTGATTCGTGAG 317
QY 21 GluLeuProArgValSerProArgPheLeuValArgAlaThrPheIleProProValSerAla 40
Db 318 GAACCTCCCGGGGTGAGCCCCCGCTTCCTCGAGCCGTGGCAACCCCTCCCGTCTCAGCC 377
QY 41 ArgMetProThrArgArgTrpAlaProGlyThrGlnCysIleThrLysCysGluHisThr 60

Db 378 AGGATGGCAACGAGGCGCTGGCCCGGGGACCCAGTGTATCAACAAATCGAGACACC 437
QY 61 ArgProLysProGlyGluLeuAlaPheArgLysGlyAspValAlaThrIleLeuAla 80
Db 438 CGCCCCAAGCCAGGGGGAGGCTGCTCCGCAAGGGGACCTGTGTACACATCCCTGGAGGCC 497
QY 81 CysGluAsnLysSerTPYrArgValLysHisIleThrSerGlyGlnGluGlyLeu 100
Db 498 TGGGAGACAGAGCTGTGTACCGGTCACACACACACAGTGACAGAGGGGCTGTG 557
QY 101 AlaAlaGlyAlaLeuArgGluArgGluAlaLeuSerAlaAspProLysLeuSerLeuMet 120
Db 558 GCAGCTGGGGCGCTGGGGGAGCGGAGGCCCTCTCCGACACCCCAAGCTCAGCTCATG 617
QY 121 ProTrpPheHisIscLysIleSerGlyGlnGluAlaValGlnGlnLeuGlnProProGlu 140
Db 618 CCGTGTTCACCGGGAAGATCTCGGGGACAGAGCTGTCCAGCAGCTGCAGCTCCCGAG 677
QY 141 AspGlyLeuPheLeuValArgGluSerAlaArgHisProGlyAspTrpValLeuCysVal 160
Db 678 GATGGCTGTTCCTGTGGGGAGTCCGGCCGACCCCGGCGHCTACGTCTGTGGTG 737
QY 161 SerPheGlyArgAspValIleHisIleTyrArgValLeuHisArgAspGlyHisLeuThrIle 180
Db 738 AGCTTGGCGCGGCGCATCCATCCAGCTGCTGACCGCGGCGGCGGCGGCGGCGGCGGCGG 797
QY 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValGlnHisIleTyrSerLysAspLys 200
Db 798 GATGAGCGCCGTGTCTCTCAACCTCATGATGATGTGGAGCATTTACACCAAGGACAG 857
QY 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGlu 220
Db 858 GCGGCTATCTGCCACCAAGCTGTGTAGACCAAGCGGAACACGGGACCAAGTGGCCGAG 917
QY 918 GAGGAGCTGGCCAGGCGGCGCTGTCTGACCTGACAGCATTTGACATTTGGGAGCACAG 977
QY 241 IleGlyGluGlyGluPheGlyAlaValLeuGlnGlyGlyThrLeuGlnLysValAla 260
Db 978 ATCGGAGAGGAGATTTGGAGCTGTCTCAGAGGTGAGTACCTGGGGGCAAAAGGTGGCC 1037
QY 261 ValLysAsnLysCysAspValThrAlaGlnAlaPheLeuAspGluThrAlaValMet 280
Db 1038 GTGAGCAATATCAAGTGTGATGTGACAGCCAGGCTTCTCGGACGAGAGCGCGTATG 1097
QY 281 ThrLysMetGlnHisGluAsnLeuValArgLeuLeuGlyAlaIleLeuHisGlnGlyLeu 300
Db 1098 ACGAAGATGCACACGAGAACTGTGTGCTCTCTGGCGGTGATCTGCACACAGGGGCTG 1157
QY 301 TyrIleValMetGluHisValSerLysGlyAsnLeuValAsnPheLeuArgThrArgGly 320
Db 1158 TACATTGTCAATGAGCAGCTGTGACCAAGGGCAACCTGTGTGAATTTCTGCGGACCCGGGGGT 1217
QY 321 ArgAlaLeuValAsnThrAlaGlnLeuGlnPheSerLeuHisValAlaGlnGlyMet 340
Db 1218 CGAGCCCTGTGAACACGCTCAGCTCTCAGCTCTCAGATTTCTGTGACGCGGGGAGGGCATG 1277
QY 341 GluTyrLeuGluSerLysLysLeuValHisArgAspLeuAlaIlaArgAsnIleLeuVal 360
Db 1278 GAGTACTGTGAGAGCAAGAACTGTGTGCACGGGAGCTGGCGCGGCGGCAATCTGTGTC 1337
QY 361 SerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGluArgLysGly 380
Db 1338 TCAGAGAGACCTGTGTGGCAAGGTACAGGACTTTGGCTGTGCCAAAGCGGAGGGG 1397
QY 381 LeuAspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLys 400
Db 1398 CTGAGACTCAAGCGCGGCTGCGCTCAAGTGGACGGCGGCGGCTCTCAACACAGGGAG 1457
QY 401 PheThrSerLysSerAspValTrpSerPheGlyValLeuLeuTrpGluValPheSerTyr 420

Db 1021 GAGTACTGAGACCAAGACCTTGTGCACCGCAGACTGGCCGCCGACATCTGTGTC 1080
Qy 361 SerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGlyArgGly 380
Db 1081 TCAGAGGACCTGGTGGCCAGAGGTCAAGACTTTGGCTTGGCCAAAGCCGAGAGGGG 1140
Qy 381 LeuAspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLys 400
Db 1141 CTAGACTCAAGCCGGCTGGCCCTCAAGTGAAGGCGCCGAGGCTCTCAAAACAGGGAG 1200
Qy 401 PheThrSerLysSerAspValTrpSerPheGlyValLeuLeuTrpGluValPheSerTyr 420
Db 1201 TTCACGACGACAGTGGATGTCTGTGAGTTTGGGGTGGCTGCTGAGAGTCTTCTCAAT 1260
Qy 421 GLYArgAlaProTyrProLysMetSerLeuLysGluValSerGluAlaValGluLysGly 440
Db 1261 GGACGGGCTCCGTACCTTAATATGTCAGTGAAGAGGTGTGGAGGCCGTGAGAGAGGG 1320
Qy 441 TyrArgMetGluProProGluGlyCysProGlyProValHisValLeuMetSerCys 460
Db 1321 TACCGCATGGAACCCCGGAGGGCTGTCCAGGCCCGCGACGTCTCATAGCAGCTGC 1380
Qy 461 TrpAlaGluArgProAlaArgArgProPheArgLysLeuAlaGluLysLeuAlaArg 480
Db 1381 TGGGAGGCAGAGCCCGCCGCGCCACCTTCGCAAACTGGCCGAGAAAGCTGGCCGG 1440
Qy 481 GluLeuArgSerAlaGlyAlaProAlaSerValSerGlyHisAspAlaAspGlySerThr 500
Db 1441 GAGCTAGCAGTGCAGGTGCCCCAGACCTCCGTCTAGGGGAGAGGCCGAGGCTCCACC 1500
Qy 501 SerProArgSerGlnGluPro 507
Db 1501 TCGCCCGCAAGCCAGAGGCC 1521

RESULT 6
US-08-876-882-1
: Sequence 1, Application US/08876882
: Patent No. 5981201
: GENERAL INFORMATION:
: APPLICANT: Abraham, Hava
: TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT
: TITLE OF INVENTION: OF BREAST CANCER
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds P. C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02173-4799
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: Windows
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/876,882
: FILING DATE: 16-JUN-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/035,228
: FILING DATE: 08-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Doreen, Hogle M
: REGISTRATION NUMBER: 36,361
: REFERENCE/DOCKET NUMBER: NEDH97-01PA
: TELEPHONE: 781-861-6240
: TELEFAX: 781-861-9540
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1987 base pairs

: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-08-876-882-1
Alignment Scores:
Pred. No.: 2,02e-249 Length: 1987
Score: 2591.50 Matches: 502
Percent Similarity: 99.21% Conservative: 1
Best Local Similarity: 99.01% Mismatches: 3
Query Match: 97.02% Indels: 3
Gaps: 1
US-09-977-260-2 (1-507) x US-08-876-882-1 (1-1987)
Qy 1 MetaLacIyArgGlySerLeuValSerTrpArgAlaPheHisGlyCysAspSerAlaGlu 20
Db 263 ATGGCGGGGAGAGCTCTGTGTTCCGTGGCGGCATTTACAGGCTGTGATTGTGTCAG 322
Qy 21 GluLeuProArgValSerProArgPheLeuArgAlaTrpHisProProProValSerAla 40
Db 323 GAACCTCCCGGGGTAGGCCCGCGCTCTCCGAGCCTGGACCCCGCCCTCCGCTCAAGCC 382
Qy 41 ArgMetProThrArgArgTrpAlaProGlyThrGlnCysIleThrLysCysGluHisThr 60
Db 383 AGGATGCCAAGAGAGCGCTGGGCCCGGCGACCCAGTGTATCACCMAATGGAGACACACC 442
Qy 61 ArgProLysProGlyGluLeuAlaPheArgLysGlyAspValValThrIleLeuGluAla 80
Db 443 CGCCCAAGCCAGGGAGAGCTGGCTCCGCAAGGGGCGACGTGTCACCATCTGAGAGGCC 502
Qy 81 CysGluAsnLysSerTrpTyrArgValLysHisHisThrSerGlyGlnGlyLeu 100
Db 503 TGCAGAAACAAGACTGTGTAACGCTCAAGCACACACCAATGAGACAGAGGGCTGTG 562
Qy 101 AlaAlaGlyAlaLeuArgGluArgGluValLeuSerAlaAspProLysLeuSerLeuMet 120
Db 563 GCACCTGGGGGCGTGGGAGAGGGAGCCCTTCCGAGACCCCAAGCTAGGCTCATG 622
Qy 121 ProTrpPheHisGlyLysIleSerGlyGlnGluAlaValGlnGlnLeuInProProGlu 140
Db 623 CCGTGTCCACAGGAAGATCTCGGCGCAGGAGCTGCCAGACCTGCACGCTCCGAG 682
Qy 141 AspGlyLeuPheLeuValArgGluSerAlaArgHisProGlyAspTyrValLeuCysVal 160
Db 683 GATGGGCTGTCCGTGGTGGAGTCCGCGCCACCCCGGAGCTAGCTGTGCTG 742
Qy 161 SerPheGlyArgAspValIleHisTyrArgValLeuHisArgAspGlyHisLeuThrIle 180
Db 743 AGCTTTGGCCCGCAGCTCATCTACCGCTGCTGCACCGCCGACGCTGCAATC 802
Qy 181 AspGluAlaValPhePheCysAsnLeuMetAspMetValGlnHisTyrSerLysAspLys 200
Db 803 GATGAGGCGCGTCTCTGCAACCTCATGAGCATGTGGAGCATTAACAGCAAGACAAAG 862
Qy 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGlu 220
Db 863 GGCCTATCTGCACCAAGCTGTGAGACCAAGCGAAACCGGAGCAATCTGGCCGAG 922
Qy 221 GluGluLeuAlaArgAlaGlyTrpLeuLeuAsnLeuGlnHisIleThrLeuGlyValGln 240
Db 923 GAGAGCTGGCGCAGGCGCGGTGTACTGAACCTGCAAGCATTTGACATTGGAGCAGAG 982
Qy 241 IleGlyGluGlyLysPheGlyAlaValLeuGlnGlyLysLysGlyGlnLysValAla 260
Db 983 ATCGAGAGGAGGAGTGTGAGCTGTCTCGAGGGTGAAGTCTCGGGGCAAAAGGTGGCC 1042
Qy 261 ValLysAsnIleLysCysAspValThrAlaGlnAlaPheLeuAspGluThrAlaValMet 280
Db 1043 GTGAAGATATCAAGTGTGATGACAGCCAGGCTTCTCGAGGAGACCGGCTCATG 1102
Qy 281 ThrLysMetGlnHisGluAsnLeuValArgLeuLeuGlyValIleLeuHisGlnGlyLeu 300

```
Db 1103 ACGAAGATGCAACACAGAACCTGGTCTCTCTGGGGTGTCTCGACACCGAGGCTG 1162
QY 301 TTTTLeValMeClnuHISValSerLysGlyAsnLeuValAsnPhenLeuArgThrArgGly 320
Db 1163 TACATTGTATGAGACAGACGTGAGCAAGGCGACACCTGTGACATTTTCTGCGACCCGGGGT 1222
QY 321 ArgAlaLeuValAsnThrAlaGlnLeuLeuGlnPheSerLeuHisValAlaGlnGlyMet 340
Db 1223 CGAGCCCTGCTGTAACACCGCTCAGCTCTGACATTTTCTGTGACGTGGCGGAGGCATG 1282
QY 341 GlnTyrLeuGlnSerLysLysLeuValHisArgAspLeuAlaAlaArgAsnIleLeuVal 360
Db 1283 GAGTACTCAAGAGCAGAGAGCTTGTGCACCGGAGCTGGCCGCCGCAACATCCGGTTC 1342
QY 361 SerGlnAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGlnArgLysGly 380
Db 1343 TCGAGAGACCTGGTGGCCAAAGTCACGACGACTTTGGCTGGCCAAAGCCGAGCGAAAGGG 1402
QY 381 LeuAspSerSerArgLeuProValLysTyrThrAlaProGlnAlaLeuLysHisGlyLys 400
Db 1403 CTGAGCTCAAGCCGCTGCCCTGCAAGTGAGCGCGCCGAGGCTCTCAAAACACGGG--- 1459
QY 401 PheThrSerLysSerAspValTyrSerPheGlyValLeuLeuTyrGlnValPheSerTyr 420
Db 1460 TTCACACGACAGCTGAGATGTGTGAGTTTGGGGTCTGCTGTGGAGAGGCTTCTCATAT 1519
QY 421 GlyArgAlaProTyrProLysMetSerLeuLysGlyValSerGlnAlaValGlnLysGly 440
Db 1520 GAGCGGGCTCCGACCTTAAATGTACATGTAAGAGAGCTGTGAGAGCCGCTGGAGAAAGGG 1579
QY 441 TyrArgMetGlnProGlnGlyCysProGlyProValHisValLeuMetSerSerCys 460
Db 1580 TACCGATGATGAACCCCGCAGAGGCTGTCCAGCGCCGCTGCACGTCTCATGACAGACTGC 1639
QY 461 TrpGlnAlaGlnProAlaArgArgProPheArgLysLysLeuAlaGlnLysLeuAlaArg 480
Db 1640 TGGAGAGCAGAGCGGCC-CGCGCGGCACCTTCGCAAACTGGCCAGAGAGCTGGCCGG 1698
QY 481 GlnLeuArgSerAlaGlyAlaProAlaSerValSerGlyGlnAspAlaAspGlySerThr 500
Db 1699 GACCTACGACAGTCCAGCTGCCCAAGCTCTGCTCAGAGGAGAGACCCGACAGCTCC-ACC 1757
QY 501 SerProArgSerGlnGlnPro 507
Db 1758 TCGCCCCGAAAGCCAGAGGCC 1778

RESULT 7
US-09-315-928-1
; Sequence 1, Application US/09315928
; Patent No. 6368796
; GENERAL INFORMATION:
; APPLICANT: Avraham, Hava
; APPLICANT: Groopman, Jerome E.
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; FILE OF INVENTION: BREAST CANCER
; FILE REFERENCE: NEDH97-01PAZ
; CURRENT APPLICATION NUMBER: US/09/315,928
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 08/876,882
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 60/035,228
; PRIOR FILING DATE: 1997-01-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)...(1846)
US-09-315-928-1
```

```
Alignment Scores:
Pred. No.: 2,02e-249 Length: 1987
Score: 2591.50 Matches: 502
Percent Similarity: 99.21% Conservative: 1
Best Local Similarity: 99.01% Mismatches: 3
Query Match: 97.02% Indels: 3
DB: 4 Gaps: 1

US-09-977-260-2 (1-507) x US-09-315-928-1 (1-1987)

QY 1 MetAlaGlyArgGlySerLeuValSerTyrPheAlaPheHisGlyCysAspSerAlaGln 20
Db 263 ATGCGGGGGAGAGCTCTGTGTTCTCTGCGGGGCAATTCACGCGTGTATTCGTGAG 322
QY 21 GlnLeuProArgValSerProArgPheLeuArgAlaThrPheProProValSerAla 40
Db 323 GAACCTTCCCGGGGTGAGCCCGCTTCTCTCGAGCTGGACCCCTCCGCTCTAGCC 382
QY 41 ArgMetProThrArgArgTyrPheAlaProGlyThrGlnCysIleThrLysCysGlnHisThr 60
Db 383 AGGATGCAACGAGGGGCTGGCCCGCGGACCCAGTGTATCAACAAATGCGAGCACACC 442
QY 61 ArgProLysProGlyGlnLeuAlaPheArgLysGlyAspValThrIleLeuGlnAla 80
Db 443 CGCCCAAGCAGAGGAGAGCTGCGCTCCGCAAGGGGACGTGTACACCATCCGAGGCC 502
QY 81 CysGlnAsnLysSerTyrTyrArgValLysHisHisThrSerGlyGlnGlnLysLeu 100
Db 503 TCGCAAGACAGAGCTGTGTCACCGCTCAGACACACACACGATGAGACAGAGGGCTGTG 562
QY 101 AlaAlaGlyAlaLeuArgGlnArgGlnAlaLeuSerAlaAspProLysLeuSerLeuMet 120
Db 563 GCAGCTGGGGCGCTGGCGGAGCGGGAGAGCCCTCTCCGACAGACCCCAAGCTCAGCTCATG 622
QY 121 ProTyrPheHisGlyLysIleSerGlyGlnGlnAlaValGlnGlnLeuGlnProProGln 140
Db 623 CCTGTGTTCACCGGAGAGCTGTGCGCCAGAGAGCTGTCCAGAGCTGACGCTCCCGAG 682
QY 141 AspGlyLeuPheLeuValArgGlnSerAlaArgHisProGlyAspTyrValLysCysVal 160
Db 683 GATGGGCTGTCTCTGTGGCGGAGTCCGCGCCGACCCCGCCACATACGTCTGTGCTG 742
QY 161 SerPheGlyArgAspValIleHisTyrArgValLeuHisArgAspGlyHisLeuThrIle 180
Db 743 AGCTTTGGCCGCGACGTCATCCATCCGCGGTCTGACGCGGACGCGCCACCTACATC 802
QY 181 AspGlnAlaValPhePheCysAsnLeuMetAspMetValGlnHisTyrSerLysAspLys 200
Db 803 GATGAGCGCGCTGTCTTCTGCAACCTCATGGACATGTGTGAGCATTAACAGCAAGGACAG 862
QY 201 GlyAlaIleCysThrLysLeuValArgProLysArgLysHisGlyThrLysSerAlaGln 220
Db 863 GCGCTATCTGCCCAACAGCTGGTGAGACCAACAGCGAAGACCGGACCAAGTGGCGGAG 922
QY 221 GlnGlnLeuAlaArgAlaGlyTyrPheLeuAsnLeuGlnHisLeuThrLeuGlnAlaGln 240
Db 923 GAGGAGCTGGCCAGGGCGGGCTGTACTGAACTGAGCATTTGACATTTGGAGACAG 982
QY 241 IleGlyGlnGlyGlnPheGlyAlaValLeuGlnGlyGlnTyrTyrLeuGlnGlnLysValAla 260
Db 983 ATCGGAGAGGAGAGTGTGGAGCTGTCTGACAGGCTGAGTACCTGGGGCAAAAGTGGCC 1042
QY 261 ValLysAsnIleLysCysAspValTyrPheAlaAlaPheLeuAspGlnThrAlaValMet 280
Db 1043 GTGAGAGATATTCAGTGTGTGACAGCCGAGCCCTTCTGACAGAGAGCGCGCTCATG 1102
QY 281 ThrLysMetGlnHisGlnLysLeuValArgLeuLeuGlyValIleLeuHisGlnGlyLeu 300
Db 1103 ACGAAGATGCAACACAGAACCTGGTCTCTCTGGGGTGTCTCGACACCGAGGCTG 1162
QY 301 TTTTLeValMeClnuHISValSerLysGlyAsnLeuValAsnPhenLeuArgThrArgGly 320
```

```

Db 1163 TACATTGTGATGAGCAGCTGAGCAGGCAACCTGTGTGAACCTTCTGCGGACCCGGGGT 1222
Qy 321 ArgAlaLeuValAsnThrAlaGlnLeuLeuGlnPheSerLeuHisValAlaGlnGlyMet 340
Db 1223 CGAGCCCTCGTGAACACCGCTCAGCTCTGACAGTTTCTCTGACGATGGCGGAGGACATG 1282
Qy 341 GlnThrLeuGlnSerLysLysLeuValHisArgAspLeuAlaAlaAsnLleLeuVal 360
Db 1283 GAGTACCTGGAGACAGAAAGCTGTGCACCGGACCTGGCGGCGCCGCAACATCTCTGTC 1342
Qy 361 SerGlnAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAlaGlnArgLysGly 380
Db 1343 TCAGAGGACCTGTGGCGCAAGGTCAGGACATTTGGCTGGCCCAAGCGGAGCGAGGAGGG 1402
Qy 381 LeuAspSerSerArgLeuProValLysThrPheAlaProGlnAlaLeuLysHisGlyLys 400
Db 1403 CTAACTCAAGCCGGCTGCGCTCAAGTGGAGGGCGCGGCTGTCAACACAGGG--- 1459
Qy 401 PheThrSerLysSerAspValTyrSerPheGlyValLeuLeuTyrGlnValAlaPheSerTyr 420
Db 1460 TTCACGACGACAGTGGATGTCTGGAGTTTGGGGTGGCTGCTGGAGGTCTTCTCANAT 1519
Qy 421 GlnArgAlaProTyrProLysMetSerLeuLysGlnValSerGlnAlaValGlnLysGly 440
Db 1520 GGAAGGGCTCCGTACCTAAATGTCACTGMAAGAGGTGTGAGGCGCTGAGAGAGGGG 1579
Qy 441 TyrArgMetGluProProGlnGlyCysProGlyProValHisValLeuMetSerSerCys 460
Db 1580 TACCGCATGAAACCCCGAGAGGCTGTCCAGGCCCCGGCGACGCTCTCATAGAGAGCTGC 1639
Qy 461 TyrGlnAlaGluProAlaArgArgProPheArgLysLeuAlaGlnLysLeuAlaArg 480
Db 1640 TGGGAGGCGAGAGCGGCC-CGGCGGCGCAACCTTCGCAACCTGGCGAGAACTGTGCCCGG 1698
Qy 481 GlnLeuArgSerAlaGlnAlaProAlaSerValSerGlyLysAspAlaAspGlySerThr 500
Db 1699 GAGTACGACAGTGCAGGTGCGCCCGACGCTCTCAGGGCGAGAGCGCGAGCGTCC-ACC 1757
Qy 501 SerProArgSerGlnGluPro 507
Db 1758 TCGCCCCGAAAGCCAGAGACC 1778

RESULT 8
US-08-604-989A-9
; Sequence 9, Application US/08604989A
; Patent No. 5834208
; GENERAL INFORMATION:
; APPLICANT: Sakano, S.
; TITLE OF INVENTION: No. 5834208el Tyrosine Kinase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604, 989A
; FILING DATE: February 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles E. Miller
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 1920-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741

```

```

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1398 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: human
; STRAIN: UT-7
; US-08-604-989A-9

Alignment Scores:
Pred. No.: 6,65e-235
Score: 2444.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 91.50%
DB: 2
Gaps: 0

US-09-977-260-2 (1-507) x US-08-604-989A-9 (1-1398)
Qy 42 MetProThrArgArgTyrPalaProGlyThrGlnCysLleThrLysCysGlnHisThrArg 61
Db 1 ATGCCAAGAGAGCGCTGGGCGCGGCGGACCCAGTGTATACCAATATGGGAGACACCGCCG 60
Qy 62 ProLysProGlyGlnLeuAlaPheArgLysLysAspValAlaThrLleLeuGlnAlaCys 81
Db 61 CCCAAGCGAGGGGAGCTGGGCTTCCGCAAGGGCGACGTGTGCACCATCTCGAGGCGCTGC 120
Qy 82 GlnAsnLysSerTyrPyrArgValLysHisThrSerGlyGlnGlnGlyLeuAla 101
Db 121 GAGAAACAGAGCTGTGACCGGCTCAAGCACCACCACTGGACAGAGGGCTGTGGCA 180
Qy 102 AlaGlnAlaLeuArgGluArgGlnAlaLeuSerAlaAspProLysLeuSerLeuMetPro 121
Db 181 GCTGGGGGCTGGCGGAGCGGAGCGGCGCCCTCTCCGACAGCCCAAGCTCAGGCTCATGGCG 240
Qy 122 TrpPheHisGlyLysLleSerGlyGlnGlnAlaValGlnGlnLeuGlnProProGluAsp 141
Db 241 TGGTTCCACGGGAGAGTCTGGGCGAGGAGCTGTCCAGCAGCTGCACCTCCCGAGAGAT 300
Qy 142 GlnLeuPheLeuValArgGlnLysArgAlaArgHisProGlyAspTyrValLeuCysValSer 161
Db 301 GGGCTGTCTCTGTGGCGGAGTCCGCGGCCACCCCGGCGACTACGTCTGTGGTGAAC 360
Qy 162 PheGlnArgAspValLleHisTyrArgValLeuHisArgAspGlnHisLeuThrLleAsp 181
Db 361 TTGGCGCGGACGTCATCCACTACCGCGTGTGCACCGCGGCGGACCTCACAATCGAT 420
Qy 182 GlnAlaValAlaPhePheCysAsnLeuMetAspMetValGlnHisTyrSerLysAspLysGly 201
Db 421 GAGGCGGTCTCTGTCAACCTCATGTGAGTGTGAGCATTCACAGCAAGCAAGAGG 480
Qy 202 AlaIleCysThrLysLeuValAlaArgProLysArgLysHisGlyThrLysSerAlaGlnGlu 221
Db 481 GCTATCTGCACCAAGCTGTGAGACCAAGCGGAAACCGGGACCAAGTCCGGCGGAGAG 540
Qy 222 GlnLeuAlaArgAlaGlyTyrPheLeuAsnLeuGlnHisLeuThrLleGlnLle 241
Db 541 GAGCTGGCGGAGGGGCGGTGTACTGAACTGCAGCATTTGACATTTGGAGCAGCATC 600
Qy 242 GlnGlnGlnGlnPheGlnAlaValLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 261
Db 601 GGAAGAGGAGAGTTTGGAGCTGTCTGAGGAGTGAATCTGGGGCAAAAGAGCGCCGTG 660
Qy 262 LysAsnLleLysCysAspValThrAlaGlnAlaPheLeuAspGlnThrAlaValMetThr 281
Db 661 AAGAATATCAAGTGTGATGTACAGCCAGGCTTTCCTGGAGCAGAGCGGCGGTCAATGCG 720
Qy 282 LysMetGlnHisGlnAsnLeuValArgLeuLeuGlnValLleLeuHisGlnGlyLeuTyr 301

```

Db 721 AAGATGCAACACAGAGAACCTGTGCTCTCTGCGGTATCTCTGACCAAGGCGCTGTAC 780
QY 302 ILeValMeTcLUhISValSerLySGlYAsnLeuValAsnPhLeuArgThrArgLyArg 321
Db 781 ATGTGATGAGACGCTGAGCAAGGAGCAACCTGTGAATTTCTGTGGAGACCCGGGGTGA 840
QY 322 AlaLeuValAsnThrArgInLeuLeuGlnPheSerLeuHisValAlaGluGlyMetGlu 341
Db 841 GCCCTGTGAAACCCCTCAGCTCCGCAAGTTTCTGTGACGCTGGCCGAGGCGCATGAG 900
QY 342 TyrLeuGluSerLySLeuValHisArgAspLeuAlaAlaArgAsnIleLeuValSer 361
Db 901 TACTGTGAGAGCAAGAGCTGTGACACCGGACCTGGCCCGCAACATCTCTGGTCTCA 960
QY 362 GluAspLeuValAlaValSerAspPheGlyLeuAlaValAlaGluArgLySGlyLeu 381
Db 961 GAGGACCTGTGGCCCAAGGTCACGACGACTTGTGGCTGGCCAAAGCCGAGCGAGGGCTTA 1020
QY 382 AspSerSerArgLeuProValLysTrpThrAlaProGluAlaLeuLysHisGlyLysPhe 401
Db 1021 GACTCAAGCGCGCTGCCCTCAAGTGCAGCGCGCCGAGGCTCTCAAAACAGGGAAGTTTC 1080
QY 402 ThrSerLySerAspValTrpSerPheGlyValLeuLeuTrpGluValPheSerTrpGly 421
Db 1081 ACCAGCAAGTCGATGTCTGAGACTTTTGGGGTCTCTCTGGAGAGTCTTCTCATATGCA 1140
QY 422 ArgAlaProLyTrpProLysMetSerLeuLysGluValSerGluAlaValGluLySGlyTyr 441
Db 1141 CGGGCTCCGTACCCCTAAATGTCAGAAAGAGTGTGAGAGCCGTGAGGAAGGGGTAC 1200
QY 442 ArgMetGluProProGluLysCysProGlyProValHisValLeuMetSerSerCysTrp 461
Db 1201 CGATGAAACCCCGCCAGGAGCTGTCCAGGCGCCGTCACGCTCTCATGAGACACTCTGTG 1260
QY 462 GluValAlaGluProAlaArgArgProPheArgLySLeuAlaGluLysLeuAlaArgLy 481
Db 1261 GAGGAGAGCCCGCCCGCGGACACCTTCCGCAAACTGGCCGAGAAAGCTGGCCCGGAG 1320
QY 482 LeuArgSerAlaGlyAlaProAlaSerValSerGlyGlnAspAlaAspGlySerThrSer 501
Db 1321 CTACGCAGTGCAGGTCCCGACGCTCCGTCTCAGGCGAGAGACCCGACGCTCCACCTCG 1380
QY 502 ProArgSerGlnGluPro 507
Db 1381 CCCCAGACCAAGGAGCC 1398
RESULT 9
US-09-741-154-1 : Sequence 1, Application US/09741154
: Patent No. 6437110
: GENERAL INFORMATION:
: APPLICANT: BEAUSLEY, Ellen M. et al
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: CLO01061
: CURRENT APPLICATION NUMBER: US/09/741,154
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 1713
: TYPE: DNA
: ORGANISM: Human
US-09-741-154-1

US-09-977-260-2 (1-507) x US-09-741-154-1 (1-1713)
QY 23 ProArgValSerPro-----ArgPheLeuAlaGlyAlaTrp 33
Db 30 CCCCAGAGACAGCGCGGCTGGCAGAGACACACAGCTGCAGGGGGCTGGAGAAAGCA 89
QY 34 HisProProProValSerAlaArgMetProThrArgArgTrpAlaProGlyThrGlnCys 53
Db 90 CACCCCTTCCTCC-----TCCCGCCAGAAACCTGCAGCCCGGAGCTTCCG--- 134
QY 54 IleThrLysCysGluHisThrArgProLysProGlyGluLeuAlaPheArgLySGlyAsp 73
Db 135 GTTGGCGA-TGC-----TGGCGCGAGCCGGG 160
QY 74 ValValThrIleLeuGluAlaCysGluAsnLysSerTrpTrpArgValLysHisThr 93
Db 161 TTGCTAGGCGACATCGAGAGAGAGAGAAAGAACTTTCATGTGGGTGCTAGAGCATCTT 220
QY 94 SerGlyGlnGluGlyLeuLeuAlaAlaGlyAlaLeuArgGluAlaAla---LeuSer 112
Db 221 AAATG-TCCCTCTCATGACAGGACATTTCCCTGTCAGACGAGAGAGAGACACCTCGGC 279
QY 113 AlaAspProLysLeu---SerLeuMetProTrpPheHisGlyLysIleSerGlyGlnGlu 131
Db 280 GAGGACCCGCTGTACAGACAGCACTTGTGTGTCCAGGGAAGATCTGGGGCCAGAG 339
QY 132 AlaValGlnGlnLeuGlnProProGluAspGlyLeuPheLeuValArgGluSerAlaArg 151
Db 340 GCTGTCCAGACAGCTGACAGCTCCCGAGAGATGGGCTTCTGCTGGCGGAGTCCGGCCG 399
QY 152 HisProGlyAspTrpValLeuCysValSerPheGlyArgAspValIleHisTrpArgVal 171
Db 400 CACCCCGGAGACTACCTCTGTGAGACTTGTGGCGGAGACTCATCCACATCCCGCTG 459
QY 172 LeuHisArgAspGlyLysLeuThrIleAspGlyAlaValPhePheCysAsnLeuMetAsp 191
Db 460 CTGCACCGGAGCGGCACCTCACAATCGATGAGGCGGTGTCTTGTGCAACCTCATAGAC 519
QY 192 MetValGlnHisTrpSerLySAspLySAlaIleCysThrLysLeuValArgProLys 211
Db 520 ATGTGTGAGACATTACAGCAAGAGCAAGGGCGCATGTGACACCAAGCTGTGAGAACCAAG 579
QY 212 ArgLysHisGlyThrLysSerAlaGluGluGlnLeuAlaArgAlaGlyTrpLeuLeuAsn 231
Db 580 CCGAAACACGGGACCAAGTCCGCCGAGAGAGACTGGCCAGGCGGCTGTACTAGAAC 639
QY 232 LeuGlnHisLeuThrLeuGlyAlaGlnIleGlyGlnGlyGlnPheGlyAlaValLeuGln 251
Db 640 CTGCACGATTTGACATTGGGAGGAGCATCGGAGAGAGAGAGTGTGGACCTGTCCGACG 699
QY 252 GlyGluTyrLeuGlnGlnLysValAlaValLysAsnIleLysCysAspValThrAlaGln 271
Db 700 GGTGAGTACTGGGGGAAAGAGTGGCGGTGAAGAAATATCAAGTGTATGTGACAGCCGAG 759
QY 272 AlaPheLeuAspGluThrAlaValMetThrLysMetGlnHisGlnAsnLeuValArgLeu 291
Db 760 GCCCTCTGAGAGAGCGCCGCTCAGAGAGATGCAACAGCAAGCACTGTGGTCTTC 819
QY 292 LeuGlyValIleLeuHisGlnGlyLeuTyrIleValMetGlnHisValSerLySGlyAsn 311
Db 820 CTGGGCGTATCTCGACCAAGGCGGTGTACATTTGTATGAGACACTGTAGCAAGGGCAAC 879
QY 312 LeuValAsnPhLeuArgThrArgGlyArgAlaLeuValAsnThrAlaGlnLeuLeuGln 331
Db 880 CTGTGTAACCTTTCTGGGAGACCCGGGGTCCAGACCTGTGAACACCCCTACGCTCGAG 939
QY 332 PheSerLeuHisValAlaGluGlyMetGluTyrLeuGlnSerLySLeuValHisArg 351
Db 940 TTTTCTCTCAGGTGGCCAGGAGCATGTGAGTCTGAGAGCAAGAACTTGTGACCCG 999
QY 352 AspLeuAlaAlaArgAsnIleLeuValSerGluAspLeuValAlaLysValSerAspPhe 371

Alignment Scores:

Pred. No.: 2,16e-192 Length: 1713
Score: 2020.50 Matches: 410
Percent Similarity: 84.88% Conservative: 11
Best Local Similarity: 82.66% Mismatches: 48
Query Match: 75.65% Indels: 29
Db: 4 Gaps: 6

```

Db      1000 GACGTGGCCGCCCGACACATCCTGGTCTCAGAGGACCTGTGTGGCCAAAGTCAGCGACTTT 1059
Qy      372  GYLEuAlaLysAlaGluArgLysGlyLeuAspSerArgLeuProValLysTrpPhe 391
Db      1060 GGCCTGGCCAAAGCCGAGGAGGAGGCTTACACTCAGACCGGGCTGCCCTCAAGTGAGCG 1119
Qy      392  AAlaProGluAlaLeuLysHisGlyLysPheThrSerLysSerAspValTrpSerPheGly 411
Db      1120 GCGCCGAGGCTCTCAACACAGGGAGAGTTTCAACAGACAGTCGGATGTGTGAGTTTGGG 1179
Qy      412  ValLeuLeuTrpGluValAlaPheSerTrpGlyArgAlaProLysProLysMetSerLeuLys 431
Db      1180 GTGCTGCTGTGGAGGCTTCTCATATGACGGGTCCGTACCTCAAAATGTCACCTGAAA 1239
Qy      432  GluValSerGluAlaValAlaGluLysGlyTyrArgMetGluProProGluGlyCysProGly 451
Db      1240 GAGGTGTGGAGGCCGTGTGAAAGAGGAGTACCGCATGAAACCCCGAGGGCTGTCTCAGGC 1299
Qy      452  ProValHisValLeuMetSerSerCysTrpGluAlaGluProAlaArgProPhe 471
Db      1300 CCCGTGCACGTCTCATGAGCAGCTGCTGGAGGAGAGCCGCCGCCGCCACCCCTTC 1359
Qy      472  ArgLysLeuAlaGluLysLeuAlaArgGluLeuArgSerAlaGlyAlaProAlaSerVal 491
Db      1360 CGCAAACTGGCCGAGAACCTGGCCCGGAGCTACGCACTGACAGTGGCCCAAGCCTCCGTC 1419
Qy      492  SerGlyLysAspAlaAspGlySerThrSerProArgSerGlnGluPro 507
Db      1420 TCAGGCGAGAGACCCCGACGCTCCACCTCGCCCGAGACCGAGAGCCC 1467

RESULT 10
US-09-741-154-3
: Sequence 3, Application US/09741154
: Patent No. 6437110
: GENERAL INFORMATION:
: APPLICANT: BEASLEY, Ellen M. et al
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
: FILE REFERENCE: CLO01061
: CURRENT APPLICATION NUMBER: US/09/741,154
: CURRENT FILING DATE: 2000-12-21
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 16389
: TYPE: DNA
: ORGANISM: Human
US-09-741-154-3

Alignment Scores:
Pred. No.: 1,03e-135 Length: 16389
Score: 1469.50 Matches: 501
Percent Similarity: 21.59% Conservative: 0
Best Local Similarity: 21.59% Mismatches: 6
Query Match: 55.02% Indels: 1819
DB: 4 Gaps: 12

US-09-977-260-2 (1-507) x US-09-741-154-3 (1-16389)
Qy      1  MetaLagLysArgLysSerLeuValSerTrpArgAlaPheHisGlyCysAspSerAlaGlu 20
Db      7229 ATGGCGGGGCGAGGCTCTGTGTTCTGCGGGGAGATTTCAGGGCTGTGATTCGTGTAG 7288
Qy      21  GLu----- 21
Db      7289 GAACCTCCCGGGTAAGATCACTTCCACAGGGGCTTGGGAGGCCAGTTCGTGGTCC 7348
Qy      21 ----- 21
Db      7349 ATCCAGGATGCTCTGTGGGAGGCTCTCTCTGCTGCCAGCATGCCCCCACCCTGACCT 7408
Qy      21 ----- 21
```

```

Db      7409 GGGCTGAAGTGTAGAGAACTGAAACCTGTGGTCCAGCCAGCCAGCTCCACCTGAGCTGTGT 7468
Qy      22  ---LeuProArgValSerProAlaPheLeuArgAlaTrpHisProProValSerAla 40
Db      7469 CCCCTCCCGAGGTG-AGCCCCCGCTTCTCCGAGCCTTG6ACCCCCCTCCGCTCAAGCC 7527
Qy      41  ArgMetProThr----- 44
Db      7528 AGGATGCCAACGGTAGTGTGTCTAGCCTGCTTCTCTGCTCCCGGGTCCCTTCTTCAAC 7587
Qy      44 ----- 44
Db      7588 TCCGTCACACCTGAGCCCTTCTCTGAAAGGGCTGTACTGTGCCCCCTACCCCTTC 7647
Qy      44 ----- 44
Db      7648 TGCTGGCCTCGGCTGGCTTCTCAGTCAATTTGGCTTCTGACCTTGTGTCCAGGC 7707
Qy      44 ----- 44
Db      7708 GCTCTCTTTGTGACTTACGATTTTCTGTGAGACACCCACTCCCTTCTTCCCC 7767
Qy      44 ----- 44
Db      7768 GATGTGTGCTGTGTTTCTGTGCTCCGCTCTTTTCAATCTTATACCTTCTGCC 7827
Qy      44 ----- 44
Db      7828 TCTGTCTCTTTCCTCCCTCCGCTCTGCTCCCAATCTCCGTATGTCCTCTT 7887
Qy      45  -----ArgArgTrpAlaProGlyThrGlnCysIleThr 56
Db      7888 GCCCTTCCCGGCCCTCTGCAAGAGCGCTGGGCCCGGACACCACTATCATACAA 7947
Qy      56  sCysGluHisThrArgProLysProGlyGluLeuAlaPheArgLysGlyAspValIleThr 76
Db      7948 ATGGAGAGACACCCGCCCAAGCAGGGGAGCTGCGCTTCGCAAGGCGAGCGTGTAC 8007
Qy      76  rIleLeuGluAlaCysGlu----- 82
Db      8008 CATCTGTGAGGCTGTCCGA-GGTGAGAGGTGCCGCGGCTGTGGCTGTGGCGTGGG 8066
Qy      83  -----As 83
Db      8067 GCTCCACGAGACCAACCCCAACACCCCACTAACCCCTGCTTCTCCCTGGACAA 8126
Qy      83  nLysSerTrpTyrArgValLysHisThrSerGlyGluGlyLeuLeuAlaIle 103
Db      8127 CAAGAGCTGTACCGCGCTCAAGACACACAGTGAAGAGGAGGCTGTGGCAGCTGG 8186
Qy      103  yAlaLeuArgLysGluArgLysAlaLeuSerAlaAspProLysLeuSerLeuMetPro----- 121
Db      8187 GCGCTGGGAGGAGGAGGCGCTCTCCGACAGCCCAAGCTCAGCTGCGGTGAGT 8246
Qy      121 ----- 121
Db      8247 GGGCAGACAGGGGCTGGGTAGGGGACAGCAAGTGAACCCCTCCACAGCCCACT 8306
Qy      122  -----TrpPheHisGlyLysIleSerGlyGluAlaVal 133
Db      8307 GACCCACCCCTTCGTGGCGCCGAGGTGTTCCAGGGGAAGTCTCGGCGAGAGGCTGT 8366
Qy      133  lGlnGluLeuGlnProProGluAspGlyLeuPheLeuValArgGluSerAlaArgHisPr 153
Db      8367 CCAGCAGCTGACGCTCCCGAGATGGCTGTCTCTGTGGGAGTCTCCGCGCCACCC 8426
Qy      153  oGlyAspTyrValLeuCysValSerPheGlyArgAspValIleHisTyrArgValLeuHis 173
Db      8427 CGCGGACTACGCTCTGTGCTGAGCTTTGGCGGAGACTCAATCACTTACCGCGTGTGCA 8486
Qy      173  sArgAspGlyHisLeuThrIleAspGluAlaValPhePheCysAsnLeuMetAspMetVal 193
```

Db 8487 CCGCCAGCGCCACTCTACAAATGAGTAGAGGCCGTTCTTCTGCAACCTCATGACATGGT 8546
QY 193 1G1u----- 194
Db 8547 GGAGGTGCTGCCACCCAGAGGGCCACCCCGTCCCTGCAGTGGGGAGGCCAGGACTCC 8606
QY 194 ----- 194
Db 8607 GGAGACTCCCTACGTAGAGATAGAGGGGCGGTCACTGACTCCATCCCTTCCCAAGC 8666
QY 194 ----- 194
Db 8667 AGCTGGGCAAGACCACTCCCTACCTCTGTCTGATACCCGGGAGCCCTCGAGCTGTGT 8726
QY 194 ----- 194
Db 8727 GCTTCCCAATGGGAGATGAAGGGGTATTCCCCAGGGGCCCCCAAGGACCCCAAGGCC 8786
QY 194 ----- 194
Db 8787 CCCATCCCATCTCAGATGGGCAAGACAGAGACCACAGATAGATTCCTTAAATGCA 8846
QY 194 ----- 194
Db 8847 GAAATAGGGGGGCTGATCCCTATGAGCTGCCCAATCTACAGTGGCTGAGTCAGCCTG 8906
QY 194 ----- 194
Db 8907 TTCTACTCCAGGAGACTAGAGTAGACTCTCTGGGGAGCCCCCAAGAACCCCAAGTTGAT 8966
QY 194 ----- 194
Db 8967 ACCAATCAGAGAGACTCCCTCTCTTTGGCTTGCTCTCCCTTCTATGAAACC 9026
QY 194 ----- 194
Db 9027 AGCCTTCTCTCTCTCCCGGTCCACCCACCCACAGAGGCCACCGGGAGCGAAC 9086
QY 195 -----H1 195
Db 9087 AGGATCTGGGGTTCCCTCCCTGGGGGTGGGCTGATGGCTGTCACCATCTGAGCA 9146
QY 195 -----H1 195
Db 9147 slytserlysasblysglyala11ecystrlylsleuValargProlysharglysh1sgl 215
|||||
Db 9147 TTACACCAAGGACAGAGGGGCTATCTGCACCAAGCTGTGAGACCAAGCGGAACACG 9206
QY 215 ythrlysserAla1glu1glu1leuAla1arg1a1----- 226
Db 9207 GACCAAGTGGGCGGAGGAGGAGCTGGCCAGGGG-TAGGGAGCGCCAGAGAGGCGAGACC 9265
QY 226 ----- 226
Db 9266 CTTTCCCTAACCCAGTTAGCCAGTCCGGGAAGGAAGGGGCTGGGGCCCCGACCTGTG 9325
QY 226 ----- 226
Db 9326 AGGCAGATCACCAAGCCTGTCTCCATGCCAGATAGGGATAGAAGACCTGGGCTGCC 9385
QY 226 ----- 226
Db 9386 TGGGGGTGCCACAGACACAGATAGTCTTTATTCAATAGSTCCCCAGCTTGGCACT 9445
QY 226 ----- 226
Db 9446 CATCTGTACATCATCACATCTGAGCCAGAAACCTGGCCCTGAACCTCCACCCACCC 9505
QY 226 ----- 226
Db 9506 CATCTGTACAGATTCCTCTTGGCCAGGTTCCCAAGACCTGGTGAATCTTCTCCCTCC 9565
QY 226 ----- 226
Db 9566 CCTCCCAACAGCCAGCTCAGGGCCTCCCATCAGACCGGCTCTTCCCAAGAGGGGAGT 9625

QY 226 ----- 226
Db 9626 CCCCTTCCAGCCAGGCGCTTGAGTGACGCTCAAGTTATCTTCTATCATGAACCAT 9685
QY 226 ----- 226
Db 9686 GCCTCCAGGAGAGAGAGGCCAGAGCTCCACCACTTCAGAACTGCTGCATGGGCTTG 9745
QY 226 ----- 226
Db 9746 AGCCACCTTCCAGCCTCATCTGCAGAAAGCCCTTCTCCACATCCACCCCTCCAGGT 9805
QY 226 ----- 226
Db 9806 CAATGTGATCATGTTTTCTTCATGCTCTGAGCCATTGTATATTCTGTCCCTTACC 9865
QY 226 ----- 226
Db 9866 TGAATGCTTTTCCAGCCCTTAAGTAGTAATCCTCAATATTAAAGTCAAAAGCAAT 9925
QY 226 ----- 226
Db 9926 GCCTCCTTGACCCCATGCTGTCTCTCTTGAAGTATCTCTCTGGGGAAGTCTGTAC 9985
QY 226 ----- 226
Db 9986 CCATCAGGGATGATCATCAGGTGAGACTAGCATCACCTGGCCATGATCTCTTAAGAC 10045
QY 226 ----- 226
Db 10046 CGTGCAATTTGGAGGGGCACTTTCTGAGGGAGAAAGAACTGTGACAAACGACCA 10105
QY 226 ----- 226
Db 10106 AGGCACTGAGGGGACAAACACAGAGTGTCTTGGAGAAAGGTCCAGGAGGCTAGAGCC 10165
QY 226 ----- 226
Db 10166 TGGAATATTCTGGAACCTTATGTGCTCCATGTGTGTTTTTGTCTGTGTGTGTT 10225
QY 226 ----- 226
Db 10226 CTGGGGTGTGACAGGTAAAGAACTGTAGGAGAGGCCAGAGGTAATTGGAGGAC 10285
QY 226 ----- 226
Db 10286 AAGAGAGCCAAAGAGAAAGGCGAGCTTATCTCTGAGAACTGAAGTGTTCCTGGCAC 10345
QY 226 ----- 226
Db 10346 TACCCCTTGGGCTGACTGAGTGGAGTCTCTGGAGGCAAGTGGGGTCTGAGGGTCTACAGC 10405
QY 226 ----- 226
Db 10406 CAGGAGGCCGCCAGCTTTGACTATTTCACACACTATCCCTCTGTAAGCCCTTTTGT 10465
QY 226 ----- 226
Db 10466 TCAAGTCAACGTGAGATAGTTCTGTGTTGCAACAACAATATTGTACAGAGAGTGGG 10525
QY 226 ----- 226
Db 10526 GTGCTGTGATATGTCTAGGGCAATGGCCAGGCCAGAGCCACTCAATGTGTATGCA 10585
QY 226 ----- 226
Db 10586 CAGCTCAGCACTGTGAGAGACATCACTAGTCTTCACCAAGTAGAAGCCCAATGGA 10645
QY 227 ----- 226
Db 10646 GGAATTTAGGGGGCCATTACCCCTGTGACTGGGCTTCACTCCACAGCGGGCTGTTACT 10705

QY	230	UAShLeuGlnHisLeuThrLeuGlyAlaGlnIleGlyGluGlyGluPheGlyAla-----	248
Db	10706	GAACCTGCACACTTTTGACATTGGGAGCAGATCGAGAGGGAGAGTTGGAGG--TGACT	10764
QY	248	-----	248
Db	10765	GGCGGACTGGGTTGGGGTCTGAGAGAGATGGAGGTGCATATTGGAGCTTTGGAGTC	10824
QY	248	-----	248
Db	10825	ACAGAGCTGAATTCAAAACCACTACTTAACCACTACTAGTTGTCAGAGCGAAGAGCTGCA	10884
QY	248	-----	248
Db	10885	AATCCTCTGAGCCCTCAGATTTCCTCCCTGTGGAGAGGGGGTAATGCGAGCTGTATGAGA	10944
QY	248	-----	248
Db	10945	GTAAGTCACTCAAGCAGCGGCTCAAGTCAAGTTAGTACTTCTTCACACTGCCAGGTC	11004
QY	248	-----	248
Db	11005	TTGTATGTGTCAGTCCCACTGTTTGGAAATGTTGAAACACCACTTCCTCGAAATTATTATTC	11064
QY	248	-----	248
Db	11065	TGGAAGCTCTGGGGTTTAAATCAGGGGTGCGACAGACTCTGTAAAGGCCAGATTGTGA	11124
QY	248	-----	248
Db	11125	AATATTCTGCTTTGTGGGCCAGTAGCTGCTGCACCACTACTGAATCTGCCCTGT	11184
QY	248	-----	248
Db	11185	GGAGTGAAGGAGCACAGACATATGTAAACATATGGGCTGGCCATGAAAACTATGAC	11244
QY	248	-----	248
Db	11245	CCAGAAATTTGAATTTTGTAAATGCTCACATGTCTGAACAGACATCATCTTTTGATT	11304
QY	248	-----	248
Db	11305	TGTTTTTACAACCATTTTAAACATGCAAAAACAGCAGCGGTGCTCATGCTGAA	11364
QY	248	-----	248
Db	11365	TCCAGACACTTTGGTAAGTGGGGCAGAGAGATCCCTTAGCTCAGAGATTCAAGTGCAG	11424
QY	248	-----	248
Db	11425	CCTGACACAGTAGCAGAGACCCCATCTGTACAAAAAAAAGCCAGCACAGATGAGCAT	11484
QY	248	-----	248
Db	11485	GCCGTAGTCCACAGCTACTCAGAGAGCGGGATGGAGAGATCCCTTGAACCCAGAAATT	11544
QY	248	-----	248
Db	11545	GAACCTCAGTGAAGCTGTGATCAGCCACTGCACCTCTACCTGGGTGAGAGAGTAGACCC	11604
QY	248	-----	248
Db	11605	TGTATCAATATTTTAAAAAATAAATATGTGGCCGGGCACAGTGGCTCATGCTGTATGC	11664
QY	248	-----	248
Db	11665	CAGCATTGGAGGCTGAGCGGGCGGATCAGAGGTCAATGAGATCGAGACATCCTGCG	11724
QY	248	-----	248
Db	11725	TAAATGTGAACCCCATCTCTACTAATAAAAAAAAAAAAAAAAAAATTAGCCGGCGCTGG	11784
QY	248	-----	248

Dd	11785	TGTTGGCGCCCTGTAGTCCACGCTACTTGGAAGCTTGAGCAGAGAAATGGCGTAGCTTG	11844
Oy	248	-----	248
Dd	11845	GGAGGCAGAGCTTGCATGATGACAGATGGCGGCACTGCATCTCACGCTTGGGCGACAGAG	11904
Oy	248	-----	248
Dd	11905	CAAGACTCCGTCTCAATAAATAATTAAATTAATTAATAAAAAATGCAAAAACAATTTT	11964
Oy	248	-----	248
Dd	11965	GAGCTGAAGGCTTTCGAAAAAGAGTGAATAGTACATTTGGCCCCGAGGGGTGGGCT	12024
Oy	248	-----	248
Dd	12025	TCACAGACCCCTGGCTTACATGGTCTCTCTTTGTTTTGTTTTTTTGTGGGGTTTTTTTT	12084
Oy	248	-----	248
Dd	12085	GAGATGAGATTTCATCTGTACACCAGCGTGAATGCAATGGCACAATCTGGCTCACGTG	12144
Oy	248	-----	248
Dd	12145	CACCTCTGCCCTCCGGGTTCAAAGTATTTCTCTGCCCTCAGCCTCCCGAGTAGTGGGAT	12204
Oy	248	-----	248
Dd	12205	TACAGGATGTGCCACACACACCTGGCTAGTTTGTATTTTCATTTAGACAGAGGTTTCTC	12264
Oy	248	-----	248
Dd	12265	CATGTAGTCGGCGCTGTCTTGAATCTGACCTCAGGTGATCCGCTGCCTCAGCCTCC	12324
Oy	248	-----	248
Dd	12325	CAAAGTCTGGGATTACAGGCGTGAGCCACCGGCCAGAGCCAGATGTTCTCTGATCTT	12384
Oy	248	-----	248
Dd	12385	GGGTCTGAGCTTGCACAGGCGGACAGGAGTGAAGAGCGGCTGTGTTCAAGTCT	12444
Oy	248	-----	248
Dd	12445	GGGAGCCCGCAGCTGTGTGAATGTTACATGGGACCGGTGTGAGCGGCTGTCCGTCTG	12504
Oy	248	-----	248
Dd	12505	TCTCTCTGTCCCCTTTGTTGGGGGTCTCATATCTCACCCCGTCCCCACCCACCCCCC	12564
Oy	249	---ValleuGlneLylutTyLeuGllylVAlAlaValLyAsnIllelyScysAs	267
Dd	12565	AGCTGCTCTCGAGGGTGAATACCTGGGGCAAAAGTGGCGGTGAAGAATATCAAGTGA	12624
Oy	267	pValThrAlaGlnAlaPheLeuaspGluThrAlaValMetThr-----	281
Dd	12625	TGTACAGACCCAGGCTTCTTGACGAGGAGCGGCGTCAATGAC-GTGAATCCACAGGTTGGG	12683
Oy	281	-----	281
Dd	12684	GCTGGGGAACCTGGGAGAGGGGGGGTCCCAAGCCCTCCACAGCCCAACCCACCCGCC	12744
Oy	282	----LysMeGlInHISgluasLeuValAr-gleuLeuGlyValIleleuHISgInglye	300
Dd	12744	CAGGAAGATCAACACACAGAACCTGTGGCTCTCTGGCGGTGATCTGCACACAGGGCT	12803
Oy	300	uTyvILleValMeGlInHISvalSerlys-----	309
Dd	12804	GTAATTTGTATGAGCACGTGACCAAGTGGGGCGGGGCCACAGCGGGGAGGGGCCCA	12863
Oy	310	-----GlyAsnLeuVa	313

Db 61 GAGTACCTGGGCAAAAGGTGGCCGTGAAGAAATATCAAGTGTGAGTGAACAGCCAGCCG 120
QY 273 PheLeuAspGluThrAlaValMetThrLysMetGlnHisGluAsnLeuValArgLeuLeu 292
Db 121 TTCCTGGAGAGAGAGCGCCCTCATGACGAAGATGCACACAGAACCTGGTGGCTTCCG 180
QY 293 GlyValIleLeuHisGlnGlyLeuTyrIleValMetGlnHisValSerLysGlyAsnLeu 312
Db 181 GGCATGATCTGCACACAGGCGGTGATCATTTGTCATGAGACAGCTGAGCAAGGCAACCTG 240
QY 313 ValAsnPheLeuArgThrArgGlyArgAlaLeuValAsnThrAlaGlnLeuGlnPhe 332
Db 241 GTGAACCTTCTGCGGACCGGGGTCTGACGCCCTGTGAACACCGCTCAGCTCCGAGTTT 300
QY 333 SerLeuHisValAlaGluGlyMetGluTyrLeuGlnSerLysLysLeuValHisAsp 352
Db 301 TCTCTCACGTGGCCAGGCGCATGAGTACCTGGAAGACAGAACGTTTGCACCCGAC 360
QY 353 LeuAlaAlaArgAsnIleLeuValSerGluAspLeuValAlaLysValSerAspPheGly 372
Db 361 CTGGCCGCGCCGCAACATCTGCTGCTCAGAGACCTGCTGGCAAGCTCAGCGACTTGGC 420
QY 373 LeuAlaLysAlaGluArgLysGlyLeuAspSerSerArgLeuProValLysTrpThrAla 392
Db 421 CTGGCCAAAGCCGAGGGAAGGGGTAGACTCAAGCGGCTGCCCTCAAGTGGAGCGGG 480
QY 393 ProGluAlaLeuLysHisGlyLysPheThrSerLysSerAspValTrpSerPheGlyVal 412
Db 481 CCGAGGCTCTCAACACCGGGAAGTTCCACGACCACTCGGATCTCGAGATTGGGGGTG 540
QY 413 LeuLeuTrpGluValPheSerTyrGlyArgAlaProTyrProLysMetSerLeuLysGlu 432
Db 541 CTGCTCTGGAGGCTTTCATATGACGAGGCTCCCTACCCCTAAATGTCACAGAAAGAG 600
QY 433 ValSerGluAlaValGluLysGlyTyrArgMetGluProProGluLysProGlyPro 452
Db 601 GTGCTCGAGCGCTGAGAAAGGGGTACCCCATGGAACCCCGAGGCGTCTCAGGCCCC 660
QY 453 ValHisValLeuMetSerCysTrpGluAlaGluProAlaArgTrpPropPheArg 472
Db 661 GTGCACGTCTCTAGACAGCTGCTGGAGGACGAGCCCGCCGCGGACCCCTTCCGC 720
QY 473 LysLeuAlaGluLysLeu 478
Db 721 AAACGTGCGGAGAGCTG 738
RESULT 12
US-07-820-011A-1
Sequence 1, Application US/07820011A
Patent No. 5336615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madril, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthinger, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasmidogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: DisplayWrite 3
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/820,011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1602 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
TITLES: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Virus
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
US-07-820-011A-1
Alignment Scores:
Pred. No.: 4,51e-64 Length: 1602
Score: 737.50 Matches: 186
Percent Similarity: 52.84% Conservative: 84
Best Local Similarity: 36.40% Mismatches: 185
Query Match: 27.61% Indels: 57
DB: 1 Gaps: 15
US-09-977-260-2 (1-507) x US-07-820-011A-1 (1-1602)
QY 23 ProArgValSerProArgPheLeuArgAlaTrpHisProProValSerAla----- 40
Db 137 CCCCAGCCGCTCT-----TTGGACCGTGGCCACCGACCCAGCTCTTGGGGCT 190
QY 41 -----ArgMetProThrArg-----TrpAlaProGly---- 50
Db 191 TCACACTTCTGACACCGTTTACCTGCCGAGCGTCCGCGGACATGGCTGC-66CGTC 249
QY 51 ThrGlnCysIleThrLysCysGlnHisThrArgProLysProGlyLysLeuAlaPheArg 70
Db 250 ACCACTTGTGCTGCTCTACGACTCAGTCCGAGTCCGAGCTGAAAGCGACTTGTCTTCAG 309
QY 71 LysGlyAspValValThrIleLeuGluAlaCysGluAsnLysSerTrpTyrArgValLys 90
Db 310 AAAGGAAGCGCTGCAGATGTCAACAACACGGAAGT---GACTGGTGGCTGCAT 366
QY 91 HisHisThrSerGlnGlnGlyLeuLeuAlaIleGlyAlaLeuArgGluArgGluAla 110
Db 367 TCCCTCATACAGACAGAGCGGCTACATCCCGAGTAATATGCGCGCCCTCAGACTCC 426
QY 111 LeuSerAlaAspProLysLeuSerLeuMetProTrpPheHisGlyLysIleSerGlyGln 130
Db 427 ATCCAGCTGAA-----GAGTGTACTTGGGGAAGATCACTCGTCGG 468
QY 131 GluAlaValGlnGlnLeuGlnProProGluAsp-----GlyLeuPheLeuValArgGlu 148
Db 469 GAGTCCGAGCGGCTGCTCTCAACCCCGAAACCCCGGGGAACCTTTTGGTCCGGAG 528
QY 149 SerAlaArgHisProGlyAspTyrValLeuCysValSer-----PheGly 163

```

Db      529  ACCGAGACGACAAAGGTGCTATTGCTCCGTTTCTGACTTTGACAAAGCCGAGGG 588
Oy      164  ArgasppVal1IleHisTyrArgValLeuHisArgAsp---GlyHisLeuThrIleAspLu 182
Db      589  CTCATGTGAGACACTACAGATCGCAAGTCGACAGCGGGCTTCTACTATCACCCTCA 648
Oy      183  AlaValPhePheCysAsnLeuMetAspMetVal1GluHisTyrSerLysAspLysGlyAla 202
Db      649  CGCACACAGTTCAGACGCTGCGACGAGCTGGGCTTACTACTCACAACATGCTGATG 708
Oy      203  IleCysThrLysLeu-----ValArpProLysArgLysHisGlyThrLysSerIleGlu 220
Db      709  TTGTCCACCGCTTACCAACAGCTCTGCCACGCTCCACGTCGACCCAGACCCAGAGGA 762
Oy      221  GluGluLeuAlaArgLag1YrPheLeuAsnLeuGlnHisLeuThrLeuGlyAlaGln 240
Db      763  -----CTCGCCAAAGAGCGGCTGGGAATCCCGCGAGAGCTGCTCGGCTGGAGGTGAG 816
Oy      241  IleGlyGluGlyGluPheGlyAlaValLeuGlnGlyGlyTyrLeuGly---GlnLysVal 259
Db      817  CTGGGGCAGGGCTGCTTGGAGAGGTCTGATGGGACCTGAGACGCGACACAGAGAGTG 876
Oy      260  AlaValLysAsnIleLys---CysAspValThrAlaGlnIlePheLeuAspGluThrAla 278
Db      877  GCCATTAAGACTCTGAAGCCCGGCAACATGTCCCGAGGCGCTTCTCGAGAGAGCCCA 936
Oy      279  ValMetThrLysMetGlnHisGluAsnLeuValArgLeuGlyValIleLeuHisGln 298
Db      937  GTGATGAAGAAGCTCGCGCATGAGAAAGCTGGTCACTGACGTGACGAGTGTGTGGAG 996
Oy      299  GlyLeuTyrIleValMetGlnHisValSerLysGlyAsnLeuValAsnPheLeuArgThr 318
Db      997  CCCATCTACATCGTCACTAGTACATGAGCAAGGGAGGACCTCTTGATTTCTCTGAAGGA 1056
Oy      319  ArgGlyArgAlaLeuValAsnThrAlaGlnLeuGlnPheSerLeuHisValAlaGlu 338
Db      1057  GAGATGGCAAGTACCTCGGCTGCCACAGCTCGCATATGGCTCGCTCAAGTTTCATCC 1116
Oy      339  GlyMetGluTyrLeuGluSerLysLysLeuValHisArgAspLeuAlaIleAspAsnIle 358
Db      1117  GGCATGGCCCTATGTGGAGAGATGAACTAGTCGACGACGAGACCTCGGCGGCCCAACTC 1176
Oy      359  LeuValSerGluAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAla----- 376
Db      1177  CTGTGGGGGAGAACCTGTGTGCAGAGGTGGCTGACTTTGGGTGGACCGCTCATCGAG 1236
Oy      377  -----GluArgGlyGlyLeuAspSerSerArgLeuProValLysThrThrAlaProGlu 394
Db      1237  GACAAAGAGTACACAGCAGCGCAAGGTCCAGATGCCCATCAATGAGTGAACAGCCCGAG 1296
Oy      395  AlaLeuLysHisGlyLysPheThrSerLysSerAspValTyrPheSerPheGlyValLeuLeu 414
Db      1297  GCAGCCCTCTATGGCGGGTTCACCATCAATGTCGATGTCTGTCTTGGCATCCTGTG 1356
Oy      415  TrpGluValPheSerTyrGlyArgAlaProTyrProLysMetSerLeuLysGluValSer 434
Db      1357  ACTGAGCTGACCAACAGCGCGGGTGCATACCCAGGAGGATGCAACAGGAGGTGCTG 1416
Oy      435  GluAlaValGluLysGlyTyrArgMetGluProProGluGlyCysProGlyProValHis 454
Db      1417  GACCAAGGTGAGAGGGGCTACCGCATGCGTCCCGCGCGAGTCCCGAGTCCGTGAT 1476
Oy      455  ValLeuMetSerSerCysTyrGluAlaGluProAlaArgArgProProPheArgLysLeu 474
Db      1477  GACCTCATGTGCCAGTGTCTGGCGGAGGAGACCTGAGAGGCGGCCACTTTTGAATGACTG 1536
Oy      475  AlaGluLysLeuAlaArgGluLeuArgSerAlaGlyAlaProAlaSerValSerGlyGln 494
Db      1537  CAGGCTTCTCTG-----GAG 1551
Oy      495  AspAlaAspGlySerThrSerProArgSerGln 505

```

```

Db      1552  GACTACTTACCTCGACAGAGCCCGATACCAG 1584
RESULT 13
PCT-US93-00445-1
Sequence 1, Application PC/TUS9300445
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madril, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 760 Kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/820,011
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-101PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1602 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANIT-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV SRC
TITLE: Gene and the Mechanism for Generating the
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
PCT-US93-00445-1
Alignment Scores:
Pred. No.: 4,51e-64 Length: 1602
Score: 737.50 Matches: 186
Percent Similarity: 52.84% Conservative: 84
Best Local Similarity: 36.40% Mismatches: 185
Query Match: 27.61% Indels: 57
DB: 5 Gaps: 15
US-09-977-260-2 (1-507) x PCT-US93-00445-1 (1-1602)

```


TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 20
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.
AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Gibbs, Carol P.
AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-3

Alignment Scores:
Pred. No.: 5,11e-63 Length: 1611
Score: 727.00 Matches: 188
Percent Similarity: 49.01% Conservative: 83
Best Local Similarity: 34.00% Mismatches: 185
Query Match: 27.22% Indels: 98
DB: 1 Gaps: 15

US-09-977-260-2 (1-507) x US-07-820-011A-3 (1-1611)

QY 24 ArgValSerProAlaGpHe-----LeuAlaGlaIaTrpHisProPro----- 36
DB 14 AGAGCAAGCCCAAGGATGCCAAGCCAGCGCGCGCGAGCTGGAGCCCGCGAGAACTGCC 73
QY 37 -----Pro 37
DB 74 ACGGCGCTGGCGGGGGCGCTTCCCGCCTCGCAGAACCCCAAGCAAGCCAGCTGGCGCG 133
QY 38 ValSerAlaArgMetProThrArgTrpAlaPro----- 49
DB 134 ACGGCGCGCGGGCGCGCGAGCGGGCC-TTCGCGCGCGGGCGCGCGAGCCCAAGCTGTC 192
QY 50 -----GlyThrGlnCysIleThrIlyCysGluHisThrArgProIlyProGly 65
DB 193 GGAGGCTTCAACTCCTCGAGACACCTCACTCCCGCAGAGGGCGGGCGCTGGCGCGGT 252
QY 66 -----GluLeuAla 68
DB 253 GGAGTGACCACTTTGTGGCCCTATGACTATGAGCTTAGAGCGAGACAGACCTGTC 312

QY 69 PheArgIySGlyAspValIaThrIleLeuGluAlaCysGluAsnIlySerTrpTyArg 88
DB 313 TTCAAGAAAGCGAGCGGCTCCAGATTGTCAACACACAGAGGGA---GACTGGTGGCTG 369
QY 89 ValIySHSHSHThSerGlyGlnGluIleuLeuAlaGlyAlaLeuAlaArgIuArg 108
DB 370 GCCCAGCTGCTCAGCAGACAGACAGCTTACATCCCAAGACTACAGTGGCGCCCTCC 429
QY 109 GluAlaLeuSerAlaAspProIlyLeuSerIleuMetProTrpPheHisGlyIlySileser 128
DB 430 GACTCCATCCAGCGCTGAG-----GAGTGGTATTGGCAAGATCAC 471
QY 129 GlyIuGluAlaValGlnGlnLeuGlnProProGluAsp-----GlyLeuPheLeuVal 146
DB 472 AGACGGAGTACAGACCGGTACTCTCTCAATGCGAGAAACCCAGAGGAGCCCTTCGTG 531
QY 147 ArgGluSerAlaArgHisProGluSpruTyValIleuCysValSer----- 161
DB 532 CGAGAAAGTGAAGACCCAGAAAGGTGCTACTGCTCTCAATGCTGTGACTTGCACAAAGCC 591
QY 162 PheGlyArgAspValIleHisTyArgValIleuHisArgAsp---GlyHisLeuThrIle 180
DB 592 AAGGCGCTCAAGCTGAAGCAGTACAGATCCGCAAGCTGAGACGGCGGCTTCAATTC 651
QY 181 AspGluAlaValIaPhePheCysAsnIleuMetAspMetValGluHisTySerIlyAspIly 200
DB 652 ACCCTCCGACCCAGCTTCAACAGCTGACAGAGCTGTGGCTTACTACTCCAAACAGCC 711
QY 201 GlyAlaIleCysThrIlyLeu-----ValArgProIlyArgGluHisGlyIlyTrpIlySer 218
DB 712 GATGGCTGTGGCCAGCGCTCAGCAGCTGTGCTCCAGCTCCAAAGCCAGCTCAGGCG 771
QY 219 AlaGluGluGluLeuAlaArgAlaGlyTrpLeuLeuAsnIleuGlnHisLeuThrIleuGly 238
DB 772 -----CTGGCCAGAGATGCTGGAGATCCCTGGAGATCCCTGGAGATCCCTGGAGAT 819
QY 239 AlaGlnIleGlyGluGlyLeuPheGlyAlaValIleuGlnGlyIlyTyIleuGly---Gln 257
DB 820 GTCAAGCTGGCGCAGGCTGTGGTGGAGGTGTGATGGAGCTGAGCAAGCTCAGCAGC 879
QY 258 LysValAlaValIlyAsnIleuLys---CysAspValIleuAlaGlnAlaPheLeuAspGlu 276
DB 880 AAGGTGGCATCAAAACCTGAAGCTGGCAGATGTCCAGAGGCTTCCAGAGAG 939
QY 277 ThrAlaIleMetThrLysMetGlnHisGluAsnIleuValArgLeuLeuGlyValIleu 296
DB 940 GCCCAGCTCATAAACAGCTGAGCATGAGAGCTGTGATGATGATGATGATGATGATGAT 999
QY 297 HisGlnGlyLeuTyTrIleValIleuMetGluHisValSerLysGlyAsnIleuValAsnPheLeu 316
DB 1000 GAGGAGCCCATTTACATGCTGTCAGGAGATGATGAGCAAGGAGGAGTTGCTGAGCTTCTC 1059
QY 317 ArgThrArgGlyArgAlaLeuValAsnThrAlaGlnIleuLeuGlnPheSerIleuHisVal 336
DB 1060 AAGGGGAGACAGCAAGTACTGCGGCTGCTGAGCTGTGGATGGATGGCTGTGAGATC 1119
QY 337 AlaGluGlyMetGlyTrpLeuGluSerIlyLysLeuValHisArgAspLeuAlaIlaArg 356
DB 1120 GCGTCAGGATGCGCTAGCTGAGCGGATGAGTACGTGATGATGATGATGATGATGATGAT 1179
QY 357 AsnIleuLeuValSerGluAspLeuValAlaIlyValSerAspPheGlyLeuAlaIlyVal 376
DB 1180 AACATCTCTGGTGGAGAGAACCTGTGTGCAAAAGTGGCCGATCTTGGCTGCTGCTGCTC 1239
QY 377 -----GluArgIlySGlyLeuAspSerIleuArgLeuProValIlyTrpThrIla 392
DB 1240 ATTGAAGCAATGATGATACAGCGCGGCAAGGTGCAAAATTCCTCATGAGGAGCGCT 1299
QY 393 ProGluAlaLeuLysIleGlyLysPheThrSerIlySerAspValIlyTrpSerPheIlyVal 412
DB 1300 CCAGAAAGTGGCTTATGAGCGCTTCAACATCAAGATGAGAGTGTGTGCTTGGGATTC 1359
QY 413 LeuLeuTrpGluValPheSerTyIlyArgAlaProTyTrpIlyMetSerLeuIlyGlu 432

QY 129 GlyGlnGluAlaValGlnGlnLeuGlnProProGluAsp-----GlyLeuPheLeuVal 146
 :::|||||::: ::: ||| |||||::: ||| |||||
Db 472 AGACGGGAGTGCAGACGGGTACTGCTCAATGCAGAGAACCCGAGAGGGACCTTCCTCGAG 531
QY 147 ArgGlnSerAlaArgHisProGlyAspTyrValLeuGlyValSer----- 161
 |||||::: ||| ||| ||| |||||
Db 532 CGAGAAATGAGACACGCAAGAGGTGCTTACTGCTGCTCAAGTGTCTGACTTCGACAAACGCC 591
QY 162 PheGlyArgAspValIleHisTyrArgValLeuHisArgAsp---GlyHisLeuThrIle 180
 ||| ::: ||| |||||::: ||| |||
Db 592 AAGGCGCTCAACGTGACAGACACTACAAAGATCCGCAAGCGGAGAGGGCGCTTCACATC 651
QY 181 AspGluAlaValPhePheCysAsnLeuMetValGlnHisTyrSerLysAspLys 200
 ||| ::: ||| ::: ||| ::: |||
Db 652 ACCTCCCGCACCCACTCAACGCTGACGACGAGCTGTGGCTTACTACTCCAAACACGCGC 711
QY 201 GlyAlaIleCysThrLysLeu-----ValArgProLysArgLysHisGlyThrLysSer 218
 ::: ||| ::: ||| ||| ||| |||
Db 712 GATGGCGTGTGCCACCGCTCACACCGTGTGCCACCGTCCAGCCGACACTCAGAGGC 771
QY 219 AlaGlnGlnGluLeuAlaArgAlaGlyTyrPheLeuAsnLeuGlnHisLeuThrLeuGly 238
 |||||::: ||| ||| ::: ||| |||
Db 772 -----CTGGCCAGAGATGCTCGGAGATCCCTCGGAGATCCGCTGGCGCTCGAG 819
QY 239 AlaGlnIleGlyGlnGlyGluPheGlyAlaValLeuGlnGlyLysTyrLeuGly---Gln 257
 ::: ||| ||| ||| ||| |||
Db 820 GTCAAGCTGGGCGAGGCTGCTTGTGCGAGGTGTGATGGGACCTGGACGCTTACACAC 879
QY 258 LysValAlaValLysAsnIleLys---CysAspValThrAlaGlnAlaPheLeuAspGlu 276
 ::: ||| ||| ||| ||| |||
Db 880 AGGCTGGCATCAAAACCTGAAAGCTGACGACGATGTCTCCAGAGGCTTCTCTGCAAGAG 939
QY 277 ThrAlaValMetThrLysMetGlnHisGlnAsnLeuValArgLeuLeuGlyValIleLeu 296
 ||||| ||| ::: ||| ||| |||
Db 940 GCCCGAGTCAATGAAGACGTGAGCATGAGAAGCTGTGTCAGTTCATGCTGTGTTCA 999
QY 297 HisGlnGlyLeuTyrIleValMetLysIleValSerLysGlyAsnLeuValAsnPheLeu 316
 ::: ||| ||| ||| ||| |||
Db 1000 GAGGAGCCCATTTACATGCTACGAGTACATGAGCAAGGGGACTTGTGTCGACTTTCTC 1059
QY 317 ArgThrArgGlyArgAlaLeuValAsnThrAlaGlnLeuGlnPheSerLeuHisVal 336
 ::: ||| ||| ||| ||| |||
Db 1060 AAGGGGAGACAGCAACTACCTGGCGCTGCTGAGTGTGGACATGGCTGCTCAGATC 1119
QY 337 AlaGlnGlyMetGluTyrLeuGlnSerLysLysLeuValHisArgAspLeuAlaIleArg 356
 ||| ||| ||| ||| |||
Db 1120 GCCTCAGGCAATGCGCTGAGCGGATGAACTGACGTCCACCGGACCTTGTGTCAGGC 1179
QY 357 AsnIleLeuValSerGlnAspLeuValAlaLysValSerAspPheGlyLeuAlaLysAla 376
 ||||| ||| ||| ||| |||
Db 1180 AACATCTGTGTGGAGAACCTGTGTGCAAAAGTGGCCGACTTGTGGCTGTGCTGCGCTC 1239
QY 377 -----GluArgLysGlyLeuAspSerArgLeuProValLysThrPheAla 392
 ||| ||| ||| ||| |||
Db 1240 ATTGAAGCAATGAGTACACGGCGCGGCAAGGTGCAAAATTCCCATCAAGTGGAGCGCT 1299
QY 393 ProGlnAlaLeuLysHisGlyLysPheThrSerLysSerAspValTyrSerPheGlyVal 412
 ||||| ::: ||| ||| ||| |||
Db 1300 CCAGAAAGCTGCCCTCTATGCGCGTTCACATCAAGTGGAGCTGTGCTTGGGATC 1359
QY 413 LeuLeuTyrPglValPheSerTyrGlyArgAlaProTyrProLysMetSerLeuLysGlu 432
 ||||| ||| ::: ||| ||| |||
Db 1360 CTGCTGACTGAGCTCACCAAGAGGCGGTGCTTACCTCGGAGTGTGAACCGCGAG 1419
QY 433 ValSerGluAlaValGluLysGlyTyrArgMetGluProProGlnGlyCysProGlyPro 452
 ||| ::: ||| ||| ||| |||
Db 1420 GTGCTGGACCAAGTGGAGCGGGGCTACCGGATGCCCTGCCCGGAGTGTCCGAGTCC 1479
QY 453 ValHisValLeuMetSerCysTyrPglValAlaGluProAlaArgArgProProPheArg 472
 ::: ||| ||| ||| ||| |||
Db 1480 CTGCACGACCTCATGTGCGAGTGTGGGAAAGAGCCTGAGGAGCGGCCCATCTTCGAG 1539
QY 473 LysLeuAlaGlnLysLeuAlaArgGluLeuArgSerAlaGlyAlaProAlaSerValSer 492

Db 1540 TACCTGCAAGGCGCTTCTG----- 1557
QY 493 GlyGlnAspAlaAspGlySerThrSerProArgSerGln 505
Db 1558 ---GAGGACTTACTTCACGTCCACCGAGGCCGCTGACAG 1593

Search completed: September 13, 2003, 04:35:10
Job time : 142 secs

QY	122	AGGCTCGGCTCAGTGTGGACACCAAGCTCCCTACTCTCTGTGTGCCAGCGCGCTGGCTGTGGCA	180
Db	121	AGGCTCGGCTCAGTGTGGACACCAAGCTCCCTACTCTCTGTGTGCCAGCGCGCTGGCTGTGGCA	180
QY	181	GGCCATTTCCAGCGCTGCCGAGCTGTGACCACTTGTCTAGTGTGCCCTTCACCTGTGCTAG	240
Db	181	GGCCATTTCCAGCGCTGCCGAGCTGTGACCACTTGTCTAGTGTGCCCTTCACCTGTGCTAG	240
QY	241	TTTCCCTCTGGGGGGCGATGGCGGGGGCAGGCTCTGTGTGTTCTGTGGCGGGCAATTTTCACG	300
Db	241	TTTCCCTCTGGGGGGCGATGGCGGGGGCAGGCTCTGTGTGTTCTGTGGCGGGCAATTTTCACG	300
QY	301	GCTGTGATTTGTCTAGGAACTTCCCGGGGTAGGCCCGCGCTCTCTCCGAGGCTTGGCAAC	360
Db	301	GCTGTGATTTGTCTAGGAACTTCCCGGGGTAGGCCCGCGCTCTCTCCGAGGCTTGGCAAC	360
QY	361	CCCCCTCCGCTCAGCCAGATGCCAACGAGGCGCTGGGGCCCCGGGGCAACCCAGTATATCA	420
Db	361	CCCCCTCCGCTCAGCCAGATGCCAACGAGGCGCTGGGGCCCCGGGGCAACCCAGTATATCA	420
QY	421	CCAAATGGGACACACCCCGCCCAAGCCAGGGGAACTGTGGCTTCCGGCAAGGGCGACGTGG	480
Db	421	CCAAATGGGACACACCCCGCCCAAGCCAGGGGAACTGTGGCTTCCGGCAAGGGCGACGTGG	480
QY	481	TCACCATTCTGGAGGCTGTGCGAAGAACAAGACTGTGTACCGGGTCAAGCAACCAACACATG	540
Db	481	TCACCATTCTGGAGGCTGTGCGAAGAACAAGACTGTGTACCGGGTCAAGCAACCAACCAATG	540
QY	541	GACGAGAGGGGCTGTGTGACAGCTGGGGGCGCTGTGGGAGCGGGAGCGGCGCTCTCCGACAC	600
Db	541	GACGAGAGGGGCTGTGTGACAGCTGGGGGCGCTGTGGGAGCGGGAGCGGCGCTCTCCGACAC	600
QY	601	CCAAGCTCAGCTCATGTCCGTGTGTTCACACGGGAATATCTCGGGGCCACGAGAGGCTGTGCCAG	660
Db	601	CCAAGCTCAGCTCATGTCCGTGTGTTCACACGGGAATATCTCGGGGCCACGAGAGGCTGTGCCAG	660
QY	661	AGCTGCACCTCCCGAGGATGGGCTGTGTCTGTGTGGGTGCGGGAGTCCGGCGGCCACCCCGGCG	720
Db	661	AGCTGCACCTCCCGAGGATGGGCTGTGTCTGTGTGGGTGCGGGAGTCCGGCGGCCACCCCGGCG	720
QY	721	ACTAGCTCTGTGGCTGTGTGTGGCGCGAGCTATCCACTACCGGGTGTGGTCACCGGCG	780
Db	721	ACTAGCTCTGTGGCTGTGTGTGGCGCGAGCTATCCACTACCGGGTGTGGTCACCGGCG	780
QY	781	ACGGCACCTCACAATCGATGAGGCGGTGTCTTCTGTGCAACCTCATGTGACATGTGTGAGC	840
Db	781	ACGGCACCTCACAATCGATGAGGCGGTGTCTTCTGTGCAACCTCATGTGACATGTGTGAGC	840
QY	841	ATTACAGAACGACAAAGGGGCGCTATCTGTACACCAAGCTGTGAGACCAAAAGGGAAACAGC	900
Db	841	ATTACAGAACGACAAAGGGGCGCTATCTGTACACCAAGCTGTGAGACCAAAAGGGAAACAGC	900
QY	901	GGACCAATTCGGCGAGGAGAGAGCTGTGCGCAGGGCGGCTGTGTTACTGAACCTGTGACATTT	960
Db	901	GGACCAATTCGGCGAGGAGAGAGCTGTGCGCAGGGCGGCTGTGTTACTGAACCTGTGACATTT	960
QY	961	TGACATTGTGGAGCACATGCTCGAGAGGAGAGTTTGTGAGCTGTCTGTGAGGGTGTGATAC	1020
Db	961	TGACATTGTGGAGCACATGCTCGAGAGGAGAGTTTGTGAGCTGTCTGTGAGGGTGTGATAC	1020
QY	1021	TGGGGCAAAAGSTGGCGGTGAAGAAATTCAGATGTGATGTACAGGCCACAGGCTTTCCTGG	1080
Db	1021	TGGGGCAAAAGSTGGCGGTGAAGAAATTCAGATGTGATGTACAGGCCACAGGCTTTCCTGG	1080
QY	1081	ACGAGAGCGCGCTCATGACGAAGATGTCAACACGAGAAACCTGTGTGGTCTCTCGGGCGTGA	1140
Db	1081	ACGAGAGCGCGCGCTCATGACGAAGATGTCAACACGAGAAACCTGTGTGGTCTCTCGGGCGTGA	1140
QY	1141	TTCCTGCACACAGGGGCTGTACTTGTCTCATGTGAGCACGTAGACAAAGGGCAACTGTGTGA	1200
Db	1141	TTCCTGCACACAGGGGCTGTACTTGTCTCATGTGAGCACGTAGACAAAGGGCAACTGTGTGA	1200

QY	1201	TTCTGCGGACACCCGGGGTGCAGCCCTCCGCGAACCACCGCTCACTCTCTGAGTTTCTCTGCG	1268
Db	1201	TTCTGCGGACCCGGGGTGCAGCCCTCCGCGAACCACCGCTCACTCTCTGAGTTTCTCTGCG	1266
QY	1261	ACGTGGCCGAGGAGCATGGAGTACCTGGAGAGACAAGAACCTTGTGCACCGCACCTGGCGCG	1320
Db	1261	ACGTGGCCGAGGAGCATGGAGTACCTGGAGAGACAAGAACCTTGTGCACCGCACCTGGCGCG	1320
QY	1321	CCCGCACATCCTGGTCTCAGAGGACCTGTGTGCCAAGGCTCAGGACTTTGGCCTGGCCA	1380
Db	1321	CCCGCACATCCTGGTCTCAGAGGACCTGTGTGCCAAGGCTCAGGACTTTGGCCTGGCCA	1380
QY	1381	AAGCGACGAGAAAGGGGCTAGACGTCAACCGCGGTCCCTGTCAAGTGGACGGCGCCGACAG	1440
Db	1381	AAGCGACGAGAAAGGGGCTAGACGTCAACCGCGGTCCCTGTCAAGTGGACGGCGCCGACAG	1440
QY	1441	CTCTCAAAACACGGGAAGTTTCAACACAGCAAGTCGATGTCTGGAGTTTGGGTGCTGCTCT	1500
Db	1441	CTCTCAAAACACGGGAAGTTTCAACACAGCAAGTCGATGTCTGGAGTTTGGGTGCTGCTCT	1500
QY	1501	GGGAGGCTTCTCATATGACGCGGCTCCGTACCTTAAATGTCACTGAAGAAGTGTGCG	1560
Db	1501	GGGAGGCTTCTCATATGACGCGGCTCCGTACCTTAAATGTCACTGAAGAAGTGTGCG	1560
QY	1561	AGGCGGTGAGAAAGGGGCTACCCGATGGAACCCCGGAGGGCTGTCCAGAGCCCGCGACAG	1620
Db	1561	AGGCGGTGAGAAAGGGGCTACCCGATGGAACCCCGGAGGGCTGTCCAGAGCCCGCGACAG	1620
QY	1621	TCTCTATGAGCAGCTGTCTGGAGGACAGCCCGCCCGCGGACCACTTCCGCAAACTGG	1680
Db	1621	TCTCTATGAGCAGCTGTCTGGAGGACAGCCCGCCCGCGGACCACTTCCGCAAACTGG	1680
QY	1681	CCGAGAAAGCTGGCCCGGGAGCTAAGGCAATGACAGTGTGCCACAGCCTCGCTCAGAGGACAG	1740
Db	1681	CCGAGAAAGCTGGCCCGGGAGCTAAGGCAATGACAGTGTGCCACAGCCTCGCTCAGAGGACAG	1740
QY	1741	ACGCGAGAGGCTTCCACCTCGCCGCCCGGAAAGCCAGAGACCTTGACCCACACCGGTGGGGCCT	1800
Db	1741	ACGCGAGAGGCTTCCACCTCGCCGCCCGGAAAGCCAGAGACCTTGACCCACACCGGTGGGGCCT	1800
QY	1801	TGGCCCCAGAGAGCCGAGAGAGTGAAGAGTGGCGGTGGGGGCACTGACAGGCCAAG	1860
Db	1801	TGGCCCCAGAGAGCCGAGAGAGTGAAGAGTGGCGGTGGGGGCACTGACAGGCCAAG	1860
QY	1861	AGGGTCACGGGGGGAAGTCACTCCCTCTGTGTGCCACAGCAGGGGGCTTGGCCACACTGAGG	1920
Db	1861	AGGGTCACGGGGGGAAGTCACTCCCTCTGTGTGCCACAGCAGGGGGCTTGGCCACACTGAGG	1920
QY	1921	GGCTCTGGGCGCCCGGTGACACCCACAGACTTGGGAAGAGATGTGCGCCGATAAAGACGG	1980
Db	1921	GGCTCTGGGCGCCCGGTGACACCCACAGACTTGGGAAGAGATGTGCGCCGATAAAGACGG	1980
QY	1981	ATTCTAAGAGACTTAAAAA 2000	
Db	1981	ATTCTAAGAGACTTAAAAA 2000	

RESULT 2
 US-09-977-260-1
 Sequence 1, Application US/09977260
 Publication No. US20020192790A1
 GENERAL INFORMATION:
 APPLICANT: ULLRICH, AXEL
 APPLICANT: GISHIZKY, MIKHAIL
 APPLICANT: SURES, IRMINARD
 TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
 FILE REFERENCE: 038602/1260
 CURRENT APPLICATION NUMBER: US/09/977,260
 CURRENT FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: 08/232,545
 PRIOR FILING DATE: 1994-04-22
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1

[illegible]

SEQ ID NO 1
LENGTH: 2000
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
NAME/KEY: CDS
LOCATION: (258)..(1778)
FEATURE:
OTHER INFORMATION: Description of Unknown organism: Megakaryocyte
US-09-977-260-1

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGCTCCAAAGTGTGACAGCCGGGACCCCTCGGGGTGTGACAGCCGCTCGGGAGGCC 60
DB 1 CTCGCTCCAAAGTGTGACAGCCGGGACCCCTCGGGGTGTGACAGCCGCTCGGGAGGCC 60
QY 61 TCCGCGGG 120
DB 61 TCCGCGGG 120
QY 121 AGGCTCGGTCCAGTGGACACCAAGCTCCTACCTCTGTGACAGCCGCTGGGCTGTGGCA 180
DB 121 AGGCTCGGTCCAGTGGACACCAAGCTCCTACCTCTGTGACAGCCGCTGGGCTGTGGCA 180
QY 181 GGGCATTCACAGCGTCCCGACCTGTGACACCTGTGACAGTGTGCTCTACCTGCTCAG 240
DB 181 GGGCATTCACAGCGTCCCGACCTGTGACACCTGTGACAGTGTGCTCTACCTGCTCAG 240
QY 241 TTTCCCTCTGG 300
DB 241 TTTCCCTCTGG 300
QY 301 GCTGTGATTTGCTGAGGAAGTTCCTCCGGGTGAGCCCGCTCTCTCCGAGCGTGGAC 360
DB 301 GCTGTGATTTGCTGAGGAAGTTCCTCCGGGTGAGCCCGCTCTCTCCGAGCGTGGAC 360
QY 361 CCCCTCCCGTCTCAGCCAGATGCCAGAGGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGG 420
DB 361 CCCCTCCCGTCTCAGCCAGATGCCAGAGGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGG 420
QY 421 CCAATGGAGACACCCGGCCCAAGCCAGGGGAGCTGGCTTCGGCAAGGGGGAGCGTGG 480
DB 421 CCAATGGAGACACCCGGCCCAAGCCAGGGGAGCTGGCTTCGGCAAGGGGGAGCGTGG 480
QY 481 TCACCATCTGGAGGCTGCGAGAACAGAGCTGTACCGGTCAAGCAACACACAGTGG 540
DB 481 TCACCATCTGGAGGCTGCGAGAACAGAGCTGTACCGGTCAAGCAACACACAGTGG 540
QY 541 GACAGAGGGGGGCTGTGAGCTGGGGGGCTGGGGAGCGGGAGGGGCGCTTCGCGAGACC 600
DB 541 GACAGAGGGGGGCTGTGAGCTGGGGGGCTGGGGAGCGGGAGGGGCGCTTCGCGAGACC 600
QY 601 CCAAGCTAGGCTCTATGGCGGTGTTCCAGGGGGAATCTCGGGCCAGGAGGGCTGTCCAGC 660
DB 601 CCAAGCTAGGCTCTATGGCGGTGTTCCAGGGGGAATCTCGGGCCAGGAGGGCTGTCCAGC 660
QY 661 AGCTCAGACCTCCAGAGATGGGCTTCTCTGTGTCGGGAGTCCGCGGCCACCCGGGG 720
DB 661 AGCTCAGACCTCCAGAGATGGGCTTCTCTGTGTCGGGAGTCCGCGGCCACCCGGGG 720
QY 721 ACTAGCTCTGTGCTGAGCTTTGGCGCGAGCTCATCACTACCGCGTGTGACCGCG 780
DB 721 ACTAGCTCTGTGCTGAGCTTTGGCGCGAGCTCATCACTACCGCGTGTGACCGCG 780
QY 781 ACGGCACTCTCAATCATGATGAGCGCGTCTTCTGTCAACCTCATGACATGATGGAGC 840
DB 781 ACGGCACTCTCAATCATGATGAGCGCGTCTTCTGTCAACCTCATGACATGATGGAGC 840
QY 841 ATTACAGCAAGACAGGGCGCTATCTGACCAAGCTGTGAGACCAAGCGGAAACAGC 900

DB 841 ATTACAGCAAGACAGGGCGCTATCTGACCAAGCTGTGAGACCAAGCGGAAACAGC 900
QY 901 GGACCAAGTCCGGCCGAGAGAGTGTCCAGGGGGGCTGTACTGAACCTGCAGCATTT 960
DB 901 GGACCAAGTCCGGCCGAGAGAGTGTCCAGGGGGGCTGTACTGAACCTGCAGCATTT 960
QY 961 TGACATTTGGGAGACAGATCCGAGAGGAGATTTGGAGCTGTCTGCAAGGTGATACC 1020
DB 961 TGACATTTGGGAGACAGATCCGAGAGGAGATTTGGAGCTGTCTGCAAGGTGATACC 1020
QY 1021 TGGGCAAAAGGTGGCCGTGAAGAAATATCAAGTGTGATGTGACAGCCGAGCTTCCTG 1080
DB 1021 TGGGCAAAAGGTGGCCGTGAAGAAATATCAAGTGTGATGTGACAGCCGAGCTTCCTG 1080
QY 1081 ACGAGACGGCGCTCATGACGAAGATGCAACAGAGACCTGTGCTCTCGGGCGTGA 1140
DB 1081 ACGAGACGGCGCTCATGACGAAGATGCAACAGAGACCTGTGCTCTCGGGCGTGA 1140
QY 1141 TCTGACACAGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 TCTGACACAGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 TTTCTGCGGACCGGGGGTGGAGCCCTGCTGAACACCCGCTCAGCTCCTGCAATTTCTG 1260
DB 1201 TTTCTGCGGACCGGGGGTGGAGCCCTGCTGAACACCCGCTCAGCTCCTGCAATTTCTG 1260
QY 1261 ACGTGGCCGAGGGATGAGATCTGTGAGAGCAAGAACTGTGTGACCGCGACCTGGGG 1320
DB 1261 ACGTGGCCGAGGGATGAGATCTGTGAGAGCAAGAACTGTGTGACCGCGACCTGGGG 1320
QY 1321 CCCGCAATCCTGCTCATGAGGACCTGGTGGGCAAGGTGACGACATTTGGCGTGGCA 1380
DB 1321 CCCGCAATCCTGCTCATGAGGACCTGGTGGGCAAGGTGACGACATTTGGCGTGGCA 1380
QY 1381 AAGCCGAGCGAAGGGGCTAGACTCAGCCGCTCCCGTCAAGTGAAGCGGCGCCGAGG 1440
DB 1381 AAGCCGAGCGAAGGGGCTAGACTCAGCCGCTCCCGTCAAGTGAAGCGGCGCCGAGG 1440
QY 1441 CTCTCAAAACAGGGGAATTCACACAGCAAGTGTCTGAGATTTTGGGGTGTGCTCT 1500
DB 1441 CTCTCAAAACAGGGGAATTCACACAGCAAGTGTCTGAGATTTTGGGGTGTGCTCT 1500
QY 1501 GGGAGGCTTCTCATATGAGAGGGGCTCCGTAACCTAAATGTCATGAAGAGGTGG 1560
DB 1501 GGGAGGCTTCTCATATGAGAGGGGCTCCGTAACCTAAATGTCATGAAGAGGTGG 1560
QY 1561 AGGCGGTGAGAAAGGGGTACCGCATGAAACCCCGAGGGGCTGTCCAGGCCCGCTGAC 1620
DB 1561 AGGCGGTGAGAAAGGGGTACCGCATGAAACCCCGAGGGGCTGTCCAGGCCCGCTGAC 1620
QY 1621 TCCTCATGACAGCTGTGAGAGGACAGCCCGCCCGCGGACCTTCGCAAAACTGG 1680
DB 1621 TCCTCATGACAGCTGTGAGAGGACAGCCCGCCCGCGGACCTTCGCAAAACTGG 1680
QY 1681 TCTCATATGAGCAGCTGTGAGAGGACAGCCCGCCCGCGGACCTTCGCAAAACTGG 1740
DB 1681 TCTCATATGAGCAGCTGTGAGAGGACAGCCCGCCCGCGGACCTTCGCTAGGGACAG 1740
QY 1741 ACGCCGAGGGCTTCACCTCGCCCGAAGCGAGAGACCTTGACCCGAGCGGTGGGGCT 1800
DB 1741 ACGCCGAGGGCTTCACCTCGCCCGAAGCGAGAGACCTTGACCCGAGCGGTGGGGCT 1800
QY 1801 TGGCCCGAGAGACCGAGAGATGAGAGTGTGGGCTGTGAGACCTGACAGGCCCAAG 1860
DB 1801 TGGCCCGAGAGACCGAGAGATGAGAGTGTGGGCTGTGAGACCTGACAGGCCCAAG 1860
QY 1861 AGGCTCAAGGGGGGCAAGTCAATCTCTGTGATGACAGAGAGGCTGACCTAGAG 1920
DB 1861 AGGCTCAAGGGGGGCAAGTCAATCTCTGTGATGACAGAGAGGCTGACCTAGAG 1920
QY 1921 GGGCTGAGGGGGCGGTGAGACCCCAAGCTGTGCAAGAGTATGCGCGATTAAGAGCG 1980

```
Db 1921 GCGCTGGGGGGCCGTGGAGACCCGACCTGCGAAGATGATCGCCCGATAAAGACGG 1980
Qy 1981 ATTCTAAGACTCTAAAAA 2000
| | | | | | | | | |
Db 1981 ATTCTAAGACTCTAAAAA 2000

RESULT 3
US-09-977-261-1
; Sequence 1, Application US/09977261
; Publication No. US20030054527A1
; GENERAL INFORMATION:
; APPLICANT: ULRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977, 261
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232, 545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (258)..(1778)
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
; OTHER INFORMATION: kinase 1
US-09-977-261-1

Query Match 100.0%; Score 2000; DB 11; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGTCCAAAGTTGTGTCAGCGCGGACCGCTCGGGGTGTGTCAGCGCGGTCGCGGAGGCC 60
| | | | | | | | | |
Db 1 CTGCGTCCAAAGTTGTGTCAGCGCGGACCGCTCGGGGTGTGTCAGCGCGGTCGCGGAGGCC 60

Qy 61 TCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 120
| | | | | | | | | |
Db 61 TCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 120

Qy 121 AGGCTGGGTCCATGTCAGACCCAGCTCCCTACCTCTCTGTGTGCGACGGCGCTGGCTGTGCA 180
| | | | | | | | | |
Db 121 AGGCTGGGTCCATGTCAGACCCAGCTCCCTACCTCTCTGTGTGCGACGGCGCTGGCTGTGCA 180

Qy 181 GGCATTTCCAGCGTCCCGACCTGTGACACACTTGTGTCAGTGTGCTCTACCTGTGCTCAG 240
| | | | | | | | | |
Db 181 GGCATTTCCAGCGTCCCGACCTGTGACACACTTGTGTCAGTGTGCTCTACCTGTGCTCAG 240

Qy 241 TTTTCCCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 300
| | | | | | | | | |
Db 241 TTTTCCCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 300

Qy 301 GGTGTATTTCTGTGAGGAATTTCCCGGGGTGAGCCCGCTTCTCTCCGAGCCTGGAGC 360
| | | | | | | | | |
Db 301 GGTGTATTTCTGTGAGGAATTTCCCGGGGTGAGCCCGCTTCTCTCCGAGCCTGGAGC 360

Qy 361 CCCCTCCGCTCTCAGCGAGATGCAACAGAGGGGTGGGCGCGGGACCCAGCAGTGTCA 420
| | | | | | | | | |
Db 361 CCCCTCCGCTCTCAGCGAGATGCAACAGAGGGGTGGGCGCGGGACCCAGCAGTGTCA 420

Qy 421 CCAATGTCAGACACCCCGCCCAAGCCAGCGAGGTGGCTTCCGAAAGGCGAGCTGG 480
| | | | | | | | | |
Db 421 CCAATGTCAGACACCCCGCCCAAGCCAGCGAGGTGGCTTCCGAAAGGCGAGCTGG 480

Qy 481 TCACCATCTCTGGAGGCTGTGAGAACAGAGCTGTACCGCTTCACAGACACACAGTGG 540
| | | | | | | | | |
Db 481 TCACCATCTCTGGAGGCTGTGAGAACAGAGCTGTACCGCTTCACAGACACACAGTGG 540

Db 481 TCACCATCTCTGGAGGCTGTGAGAACAGAGCTGTACCGCTTCACAGACACACAGTGG 540
Qy 541 GACAGAGAGGGGCTGTGTGTCAGCTGGGGGCTGGCGGAGCGGAGAGGCCCTCTCCGACAGC 600
| | | | | | | | | |
Db 541 GACAGAGAGGGGCTGTGTGTCAGCTGGGGGCTGGCGGAGCGGAGAGGCCCTCTCCGACAGC 600

Qy 601 CCAAGCTCAGCTCATATGCGGTGTGTCAGCGGGAAGATCTGGGGCAGAGAGCTGTGCA 660
| | | | | | | | | |
Db 601 CCAAGCTCAGCTCATATGCGGTGTGTCAGCGGGAAGATCTGGGGCAGAGAGCTGTGCA 660

Qy 661 AGCTGCAGCTCCCGAGAGATGGGTGTCTCTGTGTGGGGAGTCCGGCGCCACCCCGCGG 720
| | | | | | | | | |
Db 661 AGCTGCAGCTCCCGAGAGATGGGTGTCTCTGTGTGGGGAGTCCGGCGCCACCCCGCGG 720

Qy 721 ACTACGCTGTGTGTGAGCTTTGGCGGACGTCATCCATCCGCGGTCTGCACCGCG 780
| | | | | | | | | |
Db 721 ACTACGCTGTGTGTGAGCTTTGGCGGACGTCATCCATCCGCGGTCTGCACCGCG 780

Qy 781 ACGGCCACCTCACATGATGAGGCGGTGTCTCTCAACCTCATGACATGGTGGAGC 840
| | | | | | | | | |
Db 781 ACGGCCACCTCACATGATGAGGCGGTGTCTCTCAACCTCATGACATGGTGGAGC 840

Qy 841 ATTACAGCAGAGAACAGGGGCTATCTGCACCAAGCTGTGTGAGAACCAAGCGAAACAGC 900
| | | | | | | | | |
Db 841 ATTACAGCAGAGAACAGGGGCTATCTGCACCAAGCTGTGTGAGAACCAAGCGAAACAGC 900

Qy 901 GGACCAAGTGGCGCGAGAGAGCTGGCGCAGGGGGGCTGGTTACTGAACCTGCAGCATT 960
| | | | | | | | | |
Db 901 GGACCAAGTGGCGCGAGAGAGCTGGCGCAGGGGGGCTGGTTACTGAACCTGCAGCATT 960

Qy 961 TGACATTTGGAGACAGATGCGAGAGAGAGTTTGGAGCTGTCTGTCAGAGGTGATACC 1020
| | | | | | | | | |
Db 961 TGACATTTGGAGACAGATGCGAGAGAGAGTTTGGAGCTGTCTGTCAGAGGTGATACC 1020

Qy 1021 TGGGGCAAAAGTGGCGGCTGTAAGATATTCAGTGTGTGACAGCCGACGCTTCTCTGG 1080
| | | | | | | | | |
Db 1021 TGGGGCAAAAGTGGCGGCTGTAAGATATTCAGTGTGTGACAGCCGACGCTTCTCTGG 1080

Qy 1081 ACGAGAGCGCGCTCATGACGAAGATGCAACAGCAGAACCTGTGCGCTCTCTGGCGCTGA 1140
| | | | | | | | | |
Db 1081 ACGAGAGCGCGCTCATGACGAAGATGCAACAGCAGAACCTGTGCGCTCTCTGGCGCTGA 1140

Qy 1141 TCCTGCACAGGGGCTGTATCTGTGTCAGACAGCTGTGACCAAGGGCACTGTGTGACT 1200
| | | | | | | | | |
Db 1141 TCCTGCACAGGGGCTGTATCTGTGTCAGACAGCTGTGACCAAGGGCACTGTGTGACT 1200

Qy 1201 TTTCTGGGAGACCCGGGGTGTGAGCCCTCGTGAACACCGCTCAGCTCTCTGCTCTGTC 1260
| | | | | | | | | |
Db 1201 TTTCTGGGAGACCCGGGGTGTGAGCCCTCGTGAACACCGCTCAGCTCTCTGCTCTGTC 1260

Qy 1261 ACGTGGCGAGGGCATGTGATCTGTGAGAGCAAGAGCTTGTGCAACCGGACCTGGCCG 1320
| | | | | | | | | |
Db 1261 ACGTGGCGAGGGCATGTGATCTGTGAGAGCAAGAGCTTGTGCAACCGGACCTGGCCG 1320

Qy 1321 CCCGCAACATCTGTGTCTCAGAGACCTGTGTGCGCAAGTGTGACGACTTTGGCTTGCCA 1380
| | | | | | | | | |
Db 1321 CCCGCAACATCTGTGTCTCAGAGACCTGTGTGCGCAAGTGTGACGACTTTGGCTTGCCA 1380

Qy 1381 AAGCGAGGGAAGGGGCTGACCTCAAGCGGGGCTCGCCGTCAGTGTGAGAGCGGCGCGAG 1440
| | | | | | | | | |
Db 1381 AAGCGAGGGAAGGGGCTGACCTCAAGCGGGGCTCGCCGTCAGTGTGAGAGCGGCGCGAG 1440

Qy 1441 CTCTCAAAACAGGGAAGTTTACCAAGCAAGTGTGTGAGTGTGAGTGTGAGGCTGTGCT 1500
| | | | | | | | | |
Db 1441 CTCTCAAAACAGGGAAGTTTACCAAGCAAGTGTGTGAGTGTGAGTGTGAGGCTGTGCT 1500

Qy 1501 GGGAGGCTTCTCATATGAGAGGGCTCCGTAACCTTAATGTCACTGAAAGAGTGTGCG 1560
| | | | | | | | | |
Db 1501 GGGAGGCTTCTCATATGAGAGGGCTCCGTAACCTTAATGTCACTGAAAGAGTGTGCG 1560

Qy 1561 AGGCGGTGTGAGAGGGGTACCGCATGTAACCCCGCGAGGGCTGTCCAGGCGCCGTGCAGC 1620
| | | | | | | | | |
Db 1561 AGGCGGTGTGAGAGGGGTACCGCATGTAACCCCGCGAGGGCTGTCCAGGCGCCGTGCAGC 1620
```


Db	1260	GCACGTGGCCGAGGGGCAATGAGTGTACCTGGAGACGACGAAGAGCTTGTGCACGCGCACTGAC	1312
QY	1319	CGCCCGCAACATCTCGTCTCTCAGAGAGACCTGGTGGCCAAAGTCTACAGCCACTTTGGCTGGC	1378
Db	1320	CGCCCGCAACATCTCGTCTCTCAGAGAGACCTGGTGGCCAAAGTCTACAGCCACTTTGGCTGGC	1379
QY	1379	CAAAAGCCGAGGGGGAAGGGGGCTAGACTCAAGCCGGGCTGGCCGTCTCAAGTGGACGGGGCCCGA	1438
Db	1380	CAAAAGCCGAGGGGGAAGGGGGCTAGACTCAAGCCGGGCTGGCCGTCTCAAGTGGACGGGGCCCGA	1439
QY	1439	GGCTCTCAAAACACGGGAAGTTTACACAGCACTCGGATGTCTGGAGTTTGGGGTGTCTCT	1498
Db	1440	GGCTCTCAAAACACGGGAAGTTTACACAGCACTCGGATGTCTGGAGTTTGGGGTGTCTCT	1499
QY	1499	CTGGGAGGTCTTCTTCATATATGGACGGGGCTCGTACCTTAATAATGTCTACTGAAGAAGTGTCTC	1558
Db	1500	CTGGGAGGTCTTCTTCATATATGGACGGGGCTCGTACCTTAATAATGTCTACTGAAGAAGTGTCTC	1559
QY	1559	GGAGGCGCGTGGAGAAGGGGCTACCGCATGGAAACCCCGAGGGGCTGTCCAGGCCCCCGTCCA	1618
Db	1560	GGAGGCGCGTGGAGAAGGGGCTACCGCATGGAAACCCCGAGGGGCTGTCCAGGCCCCCGTCCA	1619
QY	1619	CGTCTCTATGACAGCTCTGTGGAGAGGACCCCGCCGCGGACACCTTCCGCAAACT	1678
Db	1620	CGTCTCTATGACAGCTCTGTGGAGAGGACAG - CCGCCCGCGGCGCACCTTCCGCAAACT	1678
QY	1679	GGCCGAGAAAGCTGGCCCCCGGAGACTACGCAATGACAGGTGCCCCAGCTCTCGTCAAGGGCA	1738
Db	1679	GGCCGAGAAAGCTGGCCCCCGGAGACTACGCAATGACAGGTGCCCCAGCTCTCGTCAAGGGCA	1738
QY	1739	GGAGCGCGCAGCGGCTCCACCTGCGCCCGCAAGCCAGAGAGCCCTTGACCCCAACCCGGGTG - GGCG	1797
Db	1739	GGAGCGCGCAGCGG - TCCACTCTCGCCCGCAAGCGAGAGCCCTTGACCCCAACCCGGGTG	1797
QY	1798	CCTTGAGCCCGCAGAGAGACCGAGAGAGTGGAGTGGCGGTGGGGGCACTGACACAGGCCCA	1857
Db	1798	CCTTGAGCCCGCAGAGAGACCGAGAGAGTGGAGTGGCGGTGGGGGCACTGACACAGGCCCA	1857
QY	1858	AGGAGAGGTCCAGGCGGGGCAAGTCAATCTCTCGTGTGCCACAGCAGAGGGGCTGGCCACGTA	1917
Db	1858	AGGAGAGGTCCAGGCGGGGCAAGTCAATCTCTCGTGTGCCACAGCAGAGGGGCTGGCCACGTA	1917
QY	1918	GGGGGCGTGTGGGGCGGGCCGCTGGACACACCCCAACTCTGGAAAGATGATCGCCGATAAAGA	1977
Db	1918	GGGGGCGTGTGGGGCGGGCCGCTGGACACACCCCAACTCTGGAAAGATGATCGCCGATAAAGA	1977
QY	1978	CGGATTCCTAAGG 1989	
Db	1978	CGGATTCCTAAGG 1989	
RESULT 5			
US-10-187-900-1			
: Sequence 1, Application US/10187900			
: Publication No. US20030166221A1			
: GENERAL INFORMATION:			
: APPLICANT: BEASLEY, Ellen M. et al			
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC			
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES			
: TITLE OF INVENTION: THEREOF			
: FILE REFERENCE: CL001061			
: CURRENT APPLICATION NUMBER: US/10/187,900			
: CURRENT FILING DATE: 2002-07-03			
: NUMBER OF SEQ ID NOS: 4			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 1			
: LENGTH: 1713			
: TYPE: DNA			
: ORGANISM: Human			
US-10-187-900-1			
Query Match	68.8%	Score 1377:	DB 12: Length 1713:
Best Local Similarity	99.3%	Pred. No. 0:	

	Matches	1383: Conservative	0: Mismatches	10: Indels	0: Gaps	0:
QY	608	CAGCCTATGCCCGTGTGTCACGGGAGATTCGGGCCAGGAGGCTGTCCAGCACTGCA	667			
Db	297	CAGAGAGCTTTCGTGTGTTCCACGGGAGAAATCTCGGGCCAGGAGGCTGTCCAGCACTGCA	356			
QY	668	GCCCTCCGAGGATGGGCGTTCCGTGTGTGGGAGTCCGGCGGGCCAAACCCGGCGACTAGT	727			
Db	357	GCCCTCCGAGGATGGGCGTTCTGTGTGTGGGAGTCCGGCGGGCCAAACCCGGCGACTAGT	416			
QY	728	CCTGTGCTGAGACTTTTGGCCCGCAGACGTATCCACTACCGCGTGTGCAACCCGCAAGGCCA	787			
Db	417	CCTGTGCGTGAAGCTTTTGGCCCGCAGAGTCATCCACTACCGCGTGTGCAACCGCGCAAGGCCA	476			
QY	788	CCTCAACAATGATGAGGCCGTGTCTTCTGCAACCTCATGSAACATGTGAGCATTTACAG	847			
Db	477	CCTCAACAATGATGAGGCCGTGTCTTCTTCTGCAACCTCATGSAACATGTGTGAGCATTTACAG	536			
QY	848	CAAGGACAAGGGCCGTATCTGCACCAACCTGTGAGACCAAGGGGAAACACGGGACCA	907			
Db	537	CAAGGACAAGGGCCGTATCTGCACCAACCTGTGTGAGACCAAGGGGAAACACGGGACCA	596			
QY	908	GTCGGCCAGGAGAGAGCTGGCCAGGGCGGCTGTTACTGAACCTGTGACACTTTTGACATT	967			
Db	597	GTCGGCCAGGAGAGAGCTGGCCAGGGCGGCTGTGTACTGAACCTGTGACACTTTTGACATT	656			
QY	968	GGAGACACAGATCGAGAGAGGAGATTTGAGACTGTCTCTGCAAGGGGTAGTACTTGAGCA	1027			
Db	657	GGAGACACAGATCGAGAGAGGAGATTTGGAGCTGTCTCTGCAAGGGGTAGTACTTGAGCA	716			
QY	1028	AAAGTGGCCGTGAAGAAATATCAAGTGTGATGTGACACGCCAAGGCTTCTGTGACAGAC	1087			
Db	717	AAAGTGGCCGTGAAGAAATATCAAGTGTGATGTGACACGCCAAGGCTTCTGTGACAGAAC	776			
QY	1088	GGCGCTCATGACGAAGAATGCAACACGAGAACCTGGTGGCTGCTCGGCGCTGATCTGCA	1147			
Db	777	GGCGCTCATGACGAAGAATGCAACACGAGAACCTGGTGGCTCTCGGCGCGTATCTGTCA	836			
QY	1148	CCAGGGCGTGTACATTGTTCATGTGAGACAGTGAAGCAAGGGCAACCTGTGTAACCTTTGCG	1207			
Db	837	CCAGGGCGTGTACATTGTTCATGTGAGACAGTGAAGCAAGGGCAACCTGTGTGTAACCTTTGCG	896			
QY	1208	GACCCGGGGTGGAGGCCCTTCGTGAACACCGGCTCAGTCTGTGAAATTTTCTGTGACAGTGGC	1267			
Db	897	GACCCGGGGTGGAGGCCCTTCGTGAACACCGGCTCAGTCTGTGAAATTTTCTGTGACAGTGGC	956			
QY	1268	CGAGGGCATGTGAGTACCTGGAGAGACAACCTTGTGACCGCGCACTGGCGGCCCGCAA	1327			
Db	957	CGAGGGCATGTGAGTACCTGGAGAGACAACCTTGTGCAACCGCGCACTGGCGGCCCGCAA	1016			
QY	1328	CATCCTGGTCTCAGAGGACCTGTGTGGGCCAAGGTCAGGACATTTTGGCCTGGCCAAAGCCGA	1387			
Db	1017	CATCCTGGTCTCAGAGGACCTGTGTGGGCCAAGGTCAGGACATTTTGGCCTGGCCAAAGCCGA	1076			
QY	1388	GCGGAGAGGGCTAGACTCAAGCCGGGCTGCCGTCAAGTGGACGGGCGCCGAGGCTCTCAA	1447			
Db	1077	GCGGAGAGGGCTAGACTCAAGCCGGGCTGCCGTCAAGTGGAGCGGCGCCGAGGCTCTCAA	1138			
QY	1448	ACAGGGGAAGTTCAACACAGCAAGTGGAGTGTGTGGGATTTTGGGGGTGCTGTGGAGAGT	1507			
Db	1137	ACAGGGGAAGTTCAACACAGCAAGTGGAGTGTGTGGGATTTTGGGGGTGCTGTGGAGAGT	1198			
QY	1508	CTTCTCATATGTGAGGGGCTCCGTACCCCTAAATGTCACTGAAAGAGGTGTGGAGAGCCGT	1566			
Db	1197	CTTCTCATATGTGAGGGGCTCCGTACCCCTAAATGTCACTGAAAGAGGTGTGGAGAGCCGT	1256			
QY	1568	GGAGAGAGGGTACCAGCATGAAACCCCGGAGGGCTGTCCAGGGCCCGCTGCACGTCTCAT	1627			
Db	1257	GGAGAGAGGGTACCAGCATGAAACCCCGGAGGGCTGTCCAGGGCCCGCTGCACGTCTCAT	1316			
QY	1628	GAGCAGCTGTCTGGAGGAGAGAGCCCGCGCGCGGCACACCTTTCGGCAAACTTGGCCGAGAA	1687			
Db	1317	GAGCAGCTGTCTGGAGGAGAGAGCCCGCGCGCGGCACACCTTTCGGCAAACTTGGCCGAGAA	1376			

QY 1688 GCTGGCCCGGAGTACGACAGTGCAGGTGCCCCAGCCTCCGCTCTCAGGGCAGAGCCGA 1747
 |||||
 Db 1377 GCTGGCCCGGAGTACGACAGTGCAGGTGCCCCAGCCTCCGCTCTCAGGGCAGAGCCGA 1436
 |||||
 QY 1748 CGGCTCACCTCGCCCGGAGGCCAGAGCCCTGACCCACCCGGGTGGGGCCCTTGGCCCC 1807
 |||||
 Db 1437 CGGCTCACCTCGCCCGGAGGCCAGAGCCCTGACCCACCCGGGTGGGGCCCTTGGCCCC 1496
 |||||
 QY 1808 AGAGACCCGAGAGAGTGGAGAGTGGCGCTGGGGGCACTGACAGGCCCAAGAGAGGTCC 1867
 |||||
 Db 1497 AGAGACCCGAGAGAGTGGAGAGTGGCGCTGGGGGCACTGACAGGCCCAAGAGAGGTCC 1556
 |||||
 QY 1868 AGGCGGCAAGTCACTCTCCGCTGGCCACAGCAGGGGCTGGCCACGTAGGGGCTCTG 1927
 |||||
 Db 1557 AGGCGGCAAGTCACTCTCCGCTGGCCACAGCAGGGGCTGGCCACGTAGGGGCTCTG 1616
 |||||
 QY 1928 GCGCGCCGCTGGACACCCCGACACCTGCGAAGATGATCGCCGATAAAGACGATTCGA 1987
 |||||
 Db 1617 GCGCGCCGCTGGACACCCCGACACCTGCGAAGATGATCGCCGATAAAGACGATTCGA 1676
 |||||
 QY 1988 GCACTCTAAAAA 2000
 |||||
 Db 1677 GGAATAAAAAA 1689
 |||||

RESULT 6

US-09-954-531-188
 : Sequence 188, Application US/09954531
 : Patent No. US20020165180A1
 : GENERAL INFORMATION:
 : APPLICANT: Weaver, Zoe
 : TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
 : TITLE OF INVENTION: Gene Sets
 : FILE REFERENCE: 689290-77
 : CURRENT APPLICATION NUMBER: US/09/954,531
 : CURRENT FILING DATE: 2002-05-02
 : PRIOR APPLICATION NUMBER: US/60/233,133
 : PRIOR FILING DATE: 2000-09-18
 : PRIOR APPLICATION NUMBER: US/60/234,009
 : PRIOR FILING DATE: 2000-09-20
 : PRIOR APPLICATION NUMBER: US/60/234,034
 : PRIOR FILING DATE: 2000-09-20
 : PRIOR APPLICATION NUMBER: US/60/234,509
 : PRIOR FILING DATE: 2000-09-22
 : PRIOR APPLICATION NUMBER: US/60/234,567
 : PRIOR FILING DATE: 2000-09-22
 : NUMBER OF SEQ ID NOS: 1392
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 188
 : LENGTH: 2187
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-954-531-188

Query Match 27.4%; Score 547.6; DB 10; Length 2187;
 Best Local Similarity 64.9%; Pred. No. 8,3e-124;
 Matches 846; Conservative 0; Mismatches 449; Indels 9; Gaps 2;

QY 395 CTGGGCCCCGGGACCCAGTGTATCCAAATGCGAGCACCCGCCCAAGCCAGGGGA 454
 |||||
 Db 154 CTGGGCAATCCGGTACAGATGTATTGGCAATACAACTTCCAGCGCACTGCCGAGAGGA 213
 |||||
 QY 455 GCTGGCCCTCCGAGGCGCGGTGTCATCTCGAGGCGCTGCGAAGCAAGAGTGG 514
 |||||
 Db 214 CTTGCTCTCTGCAAAAGAGAGTGTCTACCATTTGTGCGTCAACCAAGCCCAACTG 273
 |||||
 QY 515 GTACCGGTCAGACACCACTGAGACAGAGAGGGGCTGTGACAGTGGGGCTGG 574
 |||||
 Db 274 GTACAAGGCA-AAAAAGAGTGGGGCGTGAAGGCACTATCCAGCAACTACGTCA 330
 |||||
 QY 575 GGAGCGGAGGCGCTCTCCGAGACCCCAAGCTCAGGCTCATGCGGTTCACAGGGGA 634
 |||||

Db 331 GAACGGGAGGCGGTGAAGGCGGTACCAAACTCAGCCTCATGCCCTTGTTCCAGGCCAA 390
 |||||
 QY 635 GATCTGGGCGCAGAGAGCTGTCCAGCAGCTGCAGCCTCCGAGGATGGGCTGTCCGT 694
 |||||
 Db 391 GATCACACGAGGAGAGGCTGTGAGCGCTTCTGTACCGCGGAGACAGGCTGTCTGTGT 450
 |||||
 QY 695 GCGGAGTCCGCGCGCCACCCCGGAGTACGTCTGCTGCTGAGTCTTGGCCCGCAGT 754
 |||||
 Db 451 GCGGAGAGGACCAACTACCCCGGAGACTACAGCTGTGCTGAGCTGCGAGCGGCAAGT 510
 |||||
 QY 755 CATCCACTACCCGCTGCTGCACCGCAGCGCCACCTCAACTCATGATGAGCCGTTCCT 814
 |||||
 Db 511 GGAGCACTACCGCATCATGTGTACATGCCAGCAACTGACATGCACAGAGGTGTACTT 570
 |||||
 QY 815 CTGCAACCTCATGACATGTGTGAGCATTTACAGCAAGACAGAGGCCCTATCTCACC 874
 |||||
 Db 571 TGAGAACCTCATGACATGTGTGAGCATTTACAGCAAGACAGAGGCCCTATCTCACC 630
 |||||
 QY 875 GCTGTGAGACCAAGCGGAAACACGAGGACCACTGCGCGAGAGAGTGGCCAGGCG 934
 |||||
 Db 631 CTTATTAACCAAGGTCATGAGAGGCGACAGTGGCGGCCAGGATGAGTTTACCCGAG 690
 |||||
 QY 935 GCGCTGTACTGACACCTGCAGCATTTGACATTTGGAGACACAGATCGGAGAGGAGTT 994
 |||||
 Db 691 CGGCTGGGCGCTGAACATGAAGAGCTGACAGCTGCTGACAGCATCGGGAAGGGGAGTT 750
 |||||
 QY 995 TGGAGCTGTCTGTGAGGCTGTGATCTGAGCGGCAAAAGTGGCGCGTGAAGATATCA 1054
 |||||
 Db 751 CGGAGAGCTGATGTGTGGGCGATTTACCGAGGGAACAAAGTCCCTCAAGTCAATTAA 810
 |||||
 QY 1055 TGATGTGACAGCCCGAGGCTCTGAGCAGACGCGCTCATGACGAAAGATGACAAACGA 1114
 |||||
 Db 811 CGAGGCGCATGTCCAGGCGCTTCTGCTGAGAGCCTCATGACGCAACTGCGGCAATG 870
 |||||
 QY 1115 GAACCTGTGTCTCTCTGCGCGTGTATCTGCACAG- - - - -GGCTGTATCTGTCTAT 1168
 |||||
 Db 871 CAACCTGTGTGTCTCTGCGCGTGTATCTGAGAGAGGCGCGCTCATCTATCTGCTAC 930
 |||||
 QY 1169 GGACACAGTGTGACAAAGGCAACCGGTGAACCTTTCTGCGGACCGCGGCTGAGGCTCGT 1228
 |||||
 Db 931 TGAATACATGGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 990
 |||||
 QY 1229 GAACACGCTCAGCTCTGCTGACATTTCTGTCACAGTGGCCGAGGAGGAGGAGGAGGAG 1288
 |||||
 Db 991 GGGGAGAGAGCTGTCTCTCAAGTCTCTGCTGATGATCTGCGAGGCAATGGAATACGTG 1050
 |||||
 QY 1289 GAGCAAGAGGCTGTGACACCGGACCTGGCCCGCCGCAACATCTGTCTGACAGAGACT 1348
 |||||
 Db 1051 GGGCAACAATTTGCTGATCGAGACCTGGCTGCCGCAATGTCTGTGTGAGAGCA 1110
 |||||
 QY 1349 GGTGGCCAAAGTGTACGCACTTTGGCTGCGCAAAAGCCGAGGAGGAGGAGGAGGAGG 1408
 |||||
 Db 1111 CGTGGCCAAAGTGTACGCACTTTGGCTGTACCAAGAGGAGGCTGCCAGACCCGAGACGGG 1170
 |||||
 QY 1409 CCGGCTGCGCCCTCAAGTGTGAGGCGCGCCGAGAGCTCTCAAAACACGCGAAGTTCA 1468
 |||||
 Db 1171 CAACCTGTGACATCAAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1230
 |||||
 QY 1469 GTGAGATGTCTGAGATTTTGGGCTGTGCTGTGAGAGGCTTCTCATATGAGAGGCTCC 1528
 |||||
 Db 1231 GTCTGAGGTGTGGAGTTTGGGAATCTTCTGTGGGAATATCTATCTTGTGGCCAGTCC 1290
 |||||
 QY 1529 GTACCTTAATATGTACGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1588
 |||||
 Db 1291 TTATTCAGAAATTTCTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1350
 |||||
 QY 1589 ACCCCGAGGAGGCTGTCCAGGCGCCGTCACAGTCTCATGAGACAGTCTGGAGGAGCA 1648
 |||||
 Db 1351 TGCCCGGAGGAGGCTGTCCAGGCGCCGTCAGTGTATGAAGTATGAAGAACTGTGCACTG 1410
 |||||
 QY 1649 GCGCGCGCGCGGCGCACCTTTCGCAAACTGTGGCGGAGAGCTGG 1692
 |||||
 Db 1411 CGCCGCGCATGCGGCGCTCTCTTCTTACAGCTTCGAGAGGAGGAGGAGGAGGAGGAG 1454
 |||||


```
RESULT 7
; Sequence 1, Application US/10298377A
; Publication No. US20030130209A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Cheresih, David A.
; APPLICANT: Paul, Robert
; APPLICANT: Elicseiri, Brian
; TITLE OF INVENTION: Method of Treatment of Myocardial
; TITLE OF INVENTION: Infarction
; FILE REFERENCE: TSRI-651.5
; CURRENT APPLICATION NUMBER: US/10/298, 377A
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 10/298, 377
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/470, 881
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 09/538, 248
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PCT/US99/11780
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087, 220
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2187
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (134)...(1486)
US-10-298-377A-1

Query Match      27.4%; Score 547.6; DB 15; Length 2187;
Best Local Similarity 64.9%; Pred. No. 8.3e-124;
Matches 846; Conservative 0; Mismatches 449; Indels 9; Gaps 2;
```

```
QY      875 GCTGTGAGACCAAGGCAACCGGACCAAGTGGCCGAGAGGAGCTGGCCAGGCG 934
        || || || || || || || || || || || || || || || || || ||
DB      631 CCTCATTTAAACAAAAGGTATGAGGAGACAGTGGGCGCCAGATGAGTTTACCGCAG 690
QY      935 GGGCTGTGTTACGTAAACCTGACAGCATTTGATGGGAGCAGAGATGGAGAGGAGTT 994
        || || || || || || || || || || || || || || || || || ||
DB      691 CGGCTGGGCTTGAACATGAAAGAGCTGACAGTGTGACAGACCATGCGGAAGGAGGAT 750
QY      995 TGGAGCTGCTGTCAGAGGTGAGTACCTGGGCGCAAAAGTGGCCGTGAAGATATCAATG 1054
        || || || || || || || || || || || || || || || || || ||
DB      751 CGGAGACGTGATGCTGGGAGATTAACGAGGAGAAACAAAGTCGCGTCAAGTGCATTAAGAA 810
QY      1055 TGAATGACAGCCAGGACCTTCTGTGACAGAGAGCGCCGTATGACCAAGATGACACGA 1114
        || || || || || || || || || || || || || || || || || ||
DB      811 CGAGCGCATGGCCCAAGGCTTCTGTGCTGAAGCTGATGACCACTGAGGATGAG 870
QY      1115 GAACCTGTTGCGCTCTGTGGGCGTGAATCTGACACG-----GGGCTGATCTGAT 1168
        || || || || || || || || || || || || || || || || || ||
DB      871 CAACCTGTGTGACAGCTCTTGGGCGTGTATCTGTGAGAGGAGAGGCGGCTTACATGCTCAC 930
QY      1169 GGAGCAGTGTAGCAAGGCAACCTGGTGAATTTCTGCGGACCCGGGCTGAGACCTCGT 1228
        || || || || || || || || || || || || || || || || || ||
DB      931 TGAGTACATGGCCAAAGGGAGCCTTGTGACATCTGCGGTCTAAGGGGTGCTCAAGTGT 990
QY      1229 GAACACCGCTCAAGCTCTGCAAGTTTCTGTGACGTGGCCGAGGCGATGAGTACTGGA 1288
        || || || || || || || || || || || || || || || || || ||
DB      991 GGGCGGAGACTGTCTCTCAAGTTCTGCTAGATGCTGCTGAGGCGCATGGAATACCTGGA 1050
QY      1289 GAGCAGAAGACTGTGCTGACCGGACCTGGCGCGCGCAACATCTGTGCTGACAGGACCT 1348
        || || || || || || || || || || || || || || || || || ||
DB      1051 GGGCAACAATTTCTGTCATGTGAGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
QY      1349 GGTGGCCAAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1408
        || || || || || || || || || || || || || || || || || ||
DB      1111 CGTGGCCAAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1170
QY      1409 CGGCTGCGCCCTCAATGAGAGGCGCGCCGAGCTCTCAAAACAGGGAATTCACACGAA 1468
        || || || || || || || || || || || || || || || || || ||
DB      1171 CAAGCTGCAAGTGTGCAATGAGAGGCGCGCTGAGGCGCTGAGAGAAATAATTTCTCACTAA 1230
QY      1469 GTGCGATGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1528
        || || || || || || || || || || || || || || || || || ||
DB      1231 GTCTGACGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1290
QY      1529 GTACCTTAATGTCACTGAAGAAGTGTGAGAGGCGCTGAGAGAGGGTACCGATGGA 1588
        || || || || || || || || || || || || || || || || || ||
DB      1291 TTATCCAAAGATTTCCCTGGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1350
QY      1589 ACCCGCCGAGGCTGTGTCAGAGCGCCCTGCAAGTCTCATGAGCAGCTGCTGGGAGGCA 1648
        || || || || || || || || || || || || || || || || || ||
DB      1351 TGCCCGCCGAGGCTGTGTCAGAGCGCCCTGCAAGTCTCATGAGCAGCTGCTGGGAGGCA 1410
QY      1649 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1692
        || || || || || || || || || || || || || || || || || ||
DB      1411 CGCGCGCATGTGGGCGCTCTCTCTACAGCTCCGAGAGCACTTG 1454

RESULT 8
US-10-177-293-87
; Sequence 87, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Ganavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
```


APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Puzstai, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 87
LENGTH: 2420
TYPE: DNA
ORGANISM: Homo sapiens
US-10-177-293-87

Query Match 27.4%: Score 547.6; DB 14; Length 2420;
Best Local Similarity 64.9%; Pred. No. 8.3e-124;
Matches 846; Conservative 0; Mismatches 449; Indels 9; Gaps 2;

QY 395 CTGGGCCCCGGGACCCAGTGTATACCAATGGACACACCCGCCCAAGCCAGGGGA 454
DB 433 CTGGCCATCCGCTGACAGATGTATTGCCAAGTACACTCCACGCACTGCCGAGCA 492
QY 455 GCTGGCTTCCGCAAGGGGACGCTGTACCATCTGTGAGGCGCTCGAGAACAGAGCTG 514
DB 493 CTTCCCTCTTGCAGAGAGAGCGTGTACCATCTGTGAGGCGCTCGAGAACAGAGCTG 552
QY 515 GTACCGGCTCAAGACACCAAGTGTGAGAGAGGGGCTGTGAGCTGGGGCGTGGC 574
DB 553 GTCAAGGCCA---AAAACAAGGTGGGGCGGTGAGGGCATCTCCAGCACTACGTCCA 609
QY 575 GGAGCGGAGGCGCTCTCCGAGACCCCAAGCTCAGCTCATGCGTGTTCACAGGGA 634
DB 610 GAACGGGAGGCGGTGAAGGCGGGGTACCAACTCAGCTCATGCGTGTTCACAGGGA 669
QY 635 GATCTGGGCGGAGAGGCTGTCCAGCAAGTGTGAGCTGTCCAGAGATGGGCTGTCTGGT 694
DB 670 GATACACAGGGAGAGGCTGTGAGCGCTTGTACCCCGGAGACAGGCGTGTCTGGT 729
QY 695 GCGGAGATCCGCGGCGCACCCGCGGACTAGCTCTGTGCTGTGAGCTTTGGCGCGAGCT 754
DB 730 GCGGAGAGACACCAACTACCCCGGAGACTACAGCTGTGCTGTGAGCTTCGACGCGAGGT 789
QY 755 CATCCACTACCGGCTGTGTGACCGCGAGCGGCGACCTCAATCATGATGAGCGGCTGTTCT 814
DB 790 GAGACACTACCGCATGTATGTCAGTCAGCAAGCTCAGCTCAGTACAGGAGGAGTACTT 849
QY 815 CTGCAACTCATGTGACATGTGTGAGCATTTACAGCAAGGAGGCGCTATCTGACACAA 874
DB 850 TGAGAACCTCATGTGAGTGTGTGAGCACTACACCTCAGACCAATGAGACTGTACCGC 909
QY 875 GCTGCTGAGACCAAGCGGAACAAGGAGCAAGTGTGAGGAGGAGGAGGAGGCGC 934
DB 910 CTTCAATTAAACCAAGGTGATGAGGAGCAGTGTGCGGCCCAAGATGATGTTCTTACCGCAG 969
QY 935 GGGCTGTTACTGAACCTGTGACATTTGACATTTGGAGACAGATCGAGAGGAGAGATT 994

DB 970 CGGCTGGGCGCTGAACATGAAGAGAGCTGCTCAGACNATCCGGAGGCGGAGATT 1029
QY 995 TGGAGCTGTCTGTGAGGCTGAGTACCTGGGGCAAAAGGTGGCGCTGAAGATATCAAGTG 1054
DB 1030 CGGAGCTGTATGTGTGGCGATTACGAGGGAACAAAGTGGCGCTCAATGATTAAGAA 1089
QY 1055 TGAATGACAGCCAGGCGCTTCTGTGAGAGACGCGGCTCATGACGAAGATGCAACGA 1114
DB 1090 CGAGCCACATGCGCCAGGCGCTTCTGTGAGAGCTCATGATGACGACACTGCGGCAATG 1149
QY 1115 GAACCTGTGTGCTGTCTGTGGCGGTGATCTGACACAG-----GGCTGATATTGTAT 1168
DB 1150 CAACCTGTGTGAGCTCTGTGGCGGTGATGAGAGAAAGGCGGCGCTCAATGATGATG 1209
QY 1169 GGAGACGTGAGCAAGGCGCAACCTGTGTGAGACTTCTGTGAGACCCGGGGGTGAGCGCTGT 1228
DB 1210 TGAATGATGAGCGGAGGCGGAGGAGTGTGAGTACTTGTGAGGAGTGTGAGTGTGAGT 1289
QY 1229 GAACACCGCTCAGCTGTCTGTGAGTGTGTGTGACAGTGTGAGCGAGGAGTGTGAGT 1288
DB 1270 GGGGAGAGACTGTCTCTCAAGTGTGTGTGTGATGTGTGTGAGCGCATGAGATACGTGGA 1329
QY 1289 GAGCAAGAGCTTGTGACACGCGACCTGTGCGCGCGCGCAACATCTGTGTGTGAGAGACT 1348
DB 1330 GGGCAACAATTTCTGTGATGAGACCTGTGCGCGCGCGCAATGTCTGTGTGTGAGAGCAA 1389
QY 1349 GGTGGCCAAAGTGTGAGCACTTTGGCGCGCGCGCAAGCGGAGGAGGCGGAGTGTGAGT 1408
DB 1390 CGTGGCCAAAGTGTGAGCACTTTGGCGCGCGCGCGCAAGCGGAGGAGGCGGAGTGTGAGT 1449
QY 1409 CCGGCTGCGGCTCAAGTGTGAGAGGCGCGCGGAGGCTGTCAACACGCGGAGTGTCAACAGCAA 1468
DB 1450 CAACCTGTGCAATGATGTGAGAGAGCGCGCTGTGAGCGCGCTGTGAGAGAGAAATTTCTCACTAA 1509
QY 1469 GTGGAATGTGTGAGATTTGGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1528
DB 1510 GTGTGAGGT 1569
QY 1529 GTACCTTAATGT 1588
DB 1570 TTATCAAGATTTCTGT 1629
QY 1589 ACCCGCGAGGCGGTGTGAGGCGCGCGGTGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1648
DB 1630 TGCGCGCGAGCGGT 1689
QY 1649 GCCCGCGCGCGCGGT 1692
DB 1690 CGCGCGCATGT 1733

RESULT 9
US-10-187-900-3
Sequence 3, Application US/10187/900
Publication No. US20030166221A1
GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M. et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
FILE REFERENCE: CLO01061
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
CURRENT APPLICATION NUMBER: US/10/187,900
CURRENT FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 16389
TYPE: DNA
ORGANISM: Human
US-10-187-900-3

Query Match 22.8%; Score 455; DB 12; Length 16389;

Best Local Similarity 100.0%; Pred. No. 3.3e-101;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1541	GTCACATAAAGAGAGTGTGCGAGGCGCTGCGAAGAGGGTACCCGATGAAACCCCGCAGGG	1600
Db	13941	GTCACATAAAGAGAGTGTGCGAGGCGCTGCGAAGAGGGTACCCGATGAAACCCCGCAGGG	14000
QY	1601	CTGTCCAGGCGCCGTGCACGTCTCATAGACAGCTCTGTGGAGGCGAGACCCGCGCGG	1660
Db	14001	CTGTCCAGGCGCCGTGCACGTCTCATAGACAGCTCTGTGGAGGCGAGACCCGCGCGG	14060
QY	1661	GCCACCCCTTCGCGAAATGCGCGAGAACTGCGCGCGGAGACTGCGAGTGCAGGTGCCCC	1720
Db	14061	GCCACCCCTTCGCGAAATGCGCGAGAACTGCGCGCGGAGACTGCGAGTGCAGGTGCCCC	14120
QY	1721	AGCCTCCGTCTCAAGGCGAGAGCACCCGACAGGCTTCACACTGAGCCGCCGAAGCGAGAGCCTTG	1780
Db	14121	AGCCTCCGTCTCAAGGCGAGAGCACCCGACAGGCTTCACACTGAGCCGCCGAAGCGAGAGCCTTG	14180
QY	1781	ACCCACACCCGGTGGGGGCTTGTGCCCCACAGACCGAGAGAGTGAAGTGGGGCGTGGG	1840
Db	14181	ACCCACACCCGGTGGGGGCTTGTGCCCCACAGAGAGAGTGAAGTGGGGCGTGGG	14240
QY	1841	GGCACATACACAGGCGCCAGAGAGGCTCCAGGCGGGGCAAGTATCTCTGATGGCCACAGC	1900
Db	14241	GGCACATACACAGGCGCCAGAGAGGCTCCAGGCGGGGCAAGTATCTCTGATGGCCACAGC	14300
QY	1901	AGGGGCTGGGCCACGTAAGGGGGCTGTGGGCGGCCGTGGACACCCGACGACTGCGAAGGA	1960
Db	14301	AGGGGCTGGGCCACGTAAGGGGGCTGTGGGCGGCCGTGGACACCCGACGACTGCGAAGGA	14360
QY	1961	TGATTCGCGGATTAAGACGGGATTCCTTAAGGACTCTTA 1995	
Db	14361	TGATTCGCGGATTAAGACGGGATTCCTTAAGGACTCTTA 14395	

```

RESULT 10
US-09-954-456-1983
? Sequence 1983, Application US/09954456
? Patent No. US20020115057A1
? GENERAL INFORMATION:
? APPLICANT: Young, Paul
? TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer
? TITLE OF INVENTION: Sels
? FILE REFERENCE: 689230-76
? CURRENT APPLICATION NUMBER: US/09/954,456
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: US/60/233,617
? PRIOR FILING DATE: 2000-09-18
? PRIOR APPLICATION NUMBER: US/60/234,052
? PRIOR FILING DATE: 2000-09-20
? PRIOR APPLICATION NUMBER: US/60/234,923
? PRIOR FILING DATE: 2000-09-25
? PRIOR APPLICATION NUMBER: US/60/235,134
? PRIOR FILING DATE: 2000-09-25
? PRIOR APPLICATION NUMBER: US/60/235,637
? PRIOR FILING DATE: 2000-09-26
? PRIOR APPLICATION NUMBER: US/60/235,638
? PRIOR FILING DATE: 2000-09-26
? PRIOR APPLICATION NUMBER: US/60/235,711
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: US/60/235,720
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: US/60/235,840
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: US/60/235,863
? PRIOR FILING DATE: 2000-09-27
? NUMBER OF SEQ ID NOS: 2276
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 1983
? LENGTH: 2015
? TYPE: DNA
? ORGANISM: Homo sapiens

```

```

US-09-954-456-1983

Query Match          9.6%;   Score 192.6;  DB 10;  Length 2015;
Best Local Similarity 54.8%;   Pred. No. 2.1e-37;
Matches 481; Conservative 0; Mismatches 369; Indels 27; Gaps 4;

```

QY	812	CTTCTGCAACCTCAATGGACATGAGGACATTTCACGACAAAGACAAAGGGCCGCTATCGAC	871
Db	750	CTTACGACACTTCGAGAGGCTGTGTGAGCACTACAAAGAAAGGGAAACGAGGGCTCTGGCA	809
QY	872	CAAGCTGGTGAGACCAAAAGCGAAACACGGACCAAGTCGGCCGACGAGAGACTGGCCAG	931
Db	810	GAACCTGTGGGTGGCCCTGECATGTCTCCAAACCCCGAAGAGCTTGGGAAAGATGGCTTG	869
QY	932	GGCGGGGTGGTTACTGAACCTGACAGCATTTGACATTTGGAGACACAGATTCGGAGAGGAGA	991
Db	870	GGAGATCCCTTGGGAAATCCCTCAAGC-----TGAGAAAGAAACTTGGAGCTGGGCA	920
QY	992	GTTTGGAGCTGTCTCGACAGGGTGAATACCTGGGCA---AAAGTGGCCGTGAAGAAATAT	1048
Db	921	GTTTGGGGAAGTCTGGATGGCCACTACAAACAGACACCAAGGTTGGCAGTGAAGACAT	980
QY	1049	CAAG---TGTTATGTGACAGCCCAAGGCTTCTTGGAGAGACAGGCGGCTCATAGCAAAAT	1107
Db	981	GAACCCAGGGAGCATGTCTGGTGGAGGGCTTCTTGGCAAGGCGCAACATGATGAAGAACTCT	1040
QY	1106	GCACACAGAGAACCTGGTGGCTCTCTCTGGGGGTGATCTCTGACACAGGGGGCTGTACATGTT	1165
Db	1041	GCACACTGTACAAAGTGTGTCTCAACTTCATACGGGTGTCTACCAAGAGGCCATCTACATCAT	1100
QY	1166	CATGAGACACGTGAGCAAGGGCAACCTGTGTAACTTTCTGCGGAGCCGGGGTCGAGCCT	1223
Db	1101	CACGAGCTTCTATGCGCCAAAGGAAACCTGTGACTGATCTGTAAAGTGTGAGGGCAGCAA	1160
QY	1226	CGTGAACACCGCTGAGCTCTCTGCAAGTTTCTCTGAGCTGGCCGAGGACATGAGATCTT	1285
Db	1161	GCAGCCATTGGCCAAAACTCATTTGACTTCTGACGCCAGATTTGACAGAGGCATAGCCTTCAT	1220
QY	1286	GGAGAGCAAGAAGCTTGTGCACCGCGACCTGGCCGCGCCGCAACATCTGTGCTCAGAGA	1345
Db	1221	CGACGAGAGAACTACATCCACCGAGACTCCGAGCTCCCAACATCTTGCTCTGCAATC	1280
QY	1346	CTGTGGTGGCCAAAGTCAAGCATTTTGGCTTGGCCCAAGC-----CGAGCGGAA	1393
Db	1281	CTGTGGTGTGAAGATTCCTGTACTTGTGGCTGGCCGGGTCTCATTTGAGCAACAGATATAC	1340
QY	1394	GGGGCTAGACTCAAGCCGGGCTGCCCTGTCAATGTGACGGCGCCGACAGCTCTCAAAACAGG	1453
Db	1341	GGCTCGGGGAAGGGGCCAAAGTTCGCCCATCAATGAGACACTCTGAAGGCATCAACTTTGG	1400
QY	1454	GAAGTTACCAACGACAGTGTGGATGTCTGGAGTTTGGGGTGTCTCTTGGGAGGTCTTCTC	1513
Db	1401	CTCTCTTCAACATCAAGTACAGACTGTGGTCTCTTGTGTATCTGTGTGATGGAGATCTGTAC	1460
QY	1514	ATATGAGAGGGGCTCTGTACCTTAATAATGTCTACTGAAGAGGTGTGCGAGGCGCGTGAGAA	1573
Db	1461	CTTAGGGCCGGATTCCTTATCCAGGAGATGTCAAAACCTGTAAATGATTCGAGCTTCTGGAGCG	1520
QY	1574	GGGGTACCGCATGTGAACCCCGCCGAGGGCTGTCCAGGCGCCCGTGCACAGTCTCATAGAGAC	1633
Db	1521	TGTATACCGGATGCTCGCCGACAGAACTGCGCCAGAGAGAGCTCTTCAAAATCATATGATCGG	1580
QY	1634	CTGTGGGAGGACAGGCCCGCCGCGGACCACTTC	1670
Db	1581	CTGCTTGGAAAAACCGTCCGGAGGAGCGAGCCGACACTTC	1617

RESULT 11
US-10-007-010-3
; Sequence 3, Application US/10007010
; Publication No. US20030125275A1
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers

Db 1590 CTGCTGGAAGAACCGTCCAGAGGAACGCCCACTTTC 1626

RESULT 14

```

US-09-870-962-12
: Sequence 12 Application US/09870962
: Patent No. US20020081290A1
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Yue, Henry
: APPLICANT: Guegler, Karl J.
: APPLICANT: Corley, Neil C.
: APPLICANT: Gorgone, Gina
: APPLICANT: Azimzai, Yalda
: APPLICANT: Lu, Alina
: TITLE OF INVENTION: Protein Kinase Homologs
: FILE REFERENCE: PF-0614 US
: CURRENT APPLICATION NUMBER: US/09/870,962
: CURRENT FILING DATE: 2001-05-30
: PRIOR APPLICATION NUMBER: 09/0420,915
: PRIOR FILING DATE: 1999-10-20
: PRIOR APPLICATION NUMBER: US 09/173,581
: PRIOR FILING DATE: 1998-10-15
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PERL Program
: SEQ ID NO 12
: LENGTH: 1574
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: _
: OTHER INFORMATION: 507669
US-09-870-962-12

```

Query Match	9.23;	Score 185;	DB 9;	Length 1574;
Best Local Similarity	56.08;	Pred. No. 1.5e-35;		
Matches 378; Conservative	0;	Mismatches 285;	Indels 12;	Gaps 1;

QY	1030	AGGTGGGCGGAGAAATATCAAGTGTATGACAGGCCAGGCGCTTCTGTGACGACAGCG	1089
Db	415	AGGAAGGCTTCATCCCTCTCAATTTTGGCCAAAGCAAGCCTGGAGGCCGACAGGCGCA	474
QY	1090	CCGTCATGACGAAAGATGCACACGAGAAACCTGTGCGTCTGGGCGGTGATCCTGCACC	1149
Db	475	ACCTCATAGAGACGCTGCACACACCGAGGCGGTGGTTCCGGCTCTAGCGTGTGGTCAACCCAG	534
QY	1150	AGGGGCGTGCATTTGTCTATGAGACAGTGCAGAAAGGCGAACCTGTGAATTTTGTCCGGA	1209
Db	535	AGCCCATCTCATCATCTACATGMAATACATGTGGAAATGGGAAGTCAATGTGATTTTCTCAAGA	594
QY	1210	CCCGGGGTGCGAGCCCTCGTGAACACCCGCTCAGCTCTGCAGATTTTCTGTGCAGCTGGCCG	1269
Db	595	CCCTTCAGGCGATCAAGTTGATGACATCAACAACACTCTGTGACATGGCAGCCCAATTTGGAG	654
QY	1270	AGGCGATGAGATACCTGTGAGAGAGCAAGACTTGTGCACCCGCGACCTGGCGCCCGCAACA	1329
Db	655	AAAGCATAGGGCATTCATTTGAAGAGCGGAAATTAATTCATCCGTGACCTTCGGGCTGCCAACA	714
QY	1330	TTCGTGCTCTGAGAGACCTGTGGCCAAAGGTACAGCACTTTGGGCTGGC-----	1378
Db	715	TTTCGTGTGTCTGACACACCTTGAGCTGCAAGATTTGCAGACTTTGGCTTAACACGCTCATTTG	774
QY	1379	-CAAAAGCCGAGAGGAGGCGCTAGACTCAACCCGGCTGCCCGTCAGATGAGAGGCGCCG	1437
Db	775	AGGACACAGAGTACACAGCCAGGAGGAGGCGGCGCAATTTCCCATTAAGGAGACAGCGCCAG	834
QY	1438	AGGCTCTCAAAACAGGGAGATTTCCACAGCAAGTGGCATGTGTGGAGTTTGGGTGCTGCG	1497
Db	835	AAAGCATTAATCAAGGAGCATTTCCATCCATCAAGTCAGATGTGTGCTTTTGGGATCTCCGC	894
QY	1498	TCTGGGAGGCTTCTCATATGAGACGGGCTCCGTACCCCTAAATGTCTCATGAAGAGGCT	1557

Db	895	TGACGGAAATTGTCAACCCACGGCCGCATCCCTTACCCAGGGATGACCAACCCGGAGGTGA	954
Qy	1558	CGGAGGCCCGTGGAGAAAGGGTTACCGCATGAAACCCCGGAGGGCTGTCCAGGCCCCCTGC	1617
Db	955	TTTCAGAACTTCTGACGAGGCTACGCGCATGCTGCGCCCTGACAACTGTCACAGGAGAGCTGT	1014
Qy	1618	ACGTGCTCATGAGCAGCTGCTGGGAGGCGAGAGCCCGCCGGCCGACCTTCCGCAAC	1677
Db	1015	ACCAACTCATAGAGCTGTGCTGGAAAGAGCGCCACAGAGAGCCGGCCACTTGTGACTGCC	1074
Qy	1678	TGGCCGAGAGAGCTGG	1692
Db	1075	TGCGCAGTGTGCTGG	1089

RESULT 15

```

US-09-967-768A-300
: Sequence 300, Application US/09967768A
: Patent No. US20020150877A1
:
: GENERAL INFORMATION:
: APPLICANT: Augustus, Meena
: TITLE OF INVENTION: Cancer Gene Determinant
: TITLE OF INVENTION: Sets
: FILE REFERENCE: 689290-72
: CURRENT APPLICATION NUMBER: US/09/967,768A
: CURRENT FILING DATE: 2001-09-28
: PRIOR APPLICATION NUMBER: US/60/236,109
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US/60/236,034
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US/60/236,111
: PRIOR FILING DATE: 2000-09-28
: NUMBER OF SEQ ID NOS: 325
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 300
:
: LENGTH: 2354
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-09-967-768A-300

```

Query Match	9.28;	Score 184.6;	DB 10;	Length 2354;
Best Local Similarity	55.38;	Pred. No. 1.9e-35;		
Matches 473; Conservative	0;	Mismatches 374;	Indels 24;	Gaps 4;

OY	827	GGACATGTTGGAGCATTTACACAGAGCAAGGGGCGCTATTCGACACCAAGCTGTGTAGACC	886
Db	807	GGAGCTGGTGCAGCATCTACATGTAGAGGTGAATGACGGGCTGTGTCAACCTGTCTAT-----	860
OY	887	AAACCGGAAACACGGGACCAAGTGGCGCCGAGAGAGAGCTGGCCACAGGCGCGGCTGTGTACT	946
Db	861	CGCGCCCTGCACACATCATGAAAGCCCAACAGCCTGGGCTTGGCCCAAGAACGCTTGGGAAAT	920
OY	947	GAACCTCGACGATTTTGACATTGGGAGCACAGATCGGAGAGGGAGATTGTGAGCTGTCTT	1006
Db	921	CAGCGCGAGCTTCATACAGCTGTGAGCGCGGCTGGCACCGGCTGCTTCGGGGAGTGTGTG	980
OY	1007	GCAGGGTAGT---ACCTGGGGCAAAAGGTGGCCGTGAAGAAATATCAA---GTGTGATGT	1066
Db	981	GCTGGGCGACGTGGAAACGGCACACTTAAGGTGGCGGTGAAGACGCTGAAGACCGGGCACCAT	1040
OY	1061	GACAGCCACGSCCTTCCTGGACAGAGACGGCGCTCATGACGAAGATGACAAACAGAGAACCT	1120
Db	1041	GTCCCCGAAAGGCTTCCTGTGGAGAGAGCCCAAGTCTATGAAGCTGCTGCGGGCACACAGCT	1100
OY	1121	GGTGCGTTCCTTGGGCGGTGATCTGTACACAGAGGGGCTGTACATTGTTCATGTGGAGACAGTGTAG	1180
Db	1101	GGTGCAGGTGTACGCGCGTGTGTGGAGAGAGCCCATCTACATCGTAGACAGAGTTATGTGTG	1160
OY	1181	CAAGGGCAACCTGTGAACCTTTTCTGTCCGAGACCCGGGGGTGAGCCCTCGTGAACACCGCTCA	1240
Db	1161	TCACGCGAGCTGTGGTGTGATTTTCTCAAGAACCCACAGAGGGCCACAGATTTGTAGAGCTGTCCCCA	1220

